

Access DB# 27709

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: W. S. Y. Cuck Examiner #: 77134 Date: 4/14/00
Art Unit: 1641 Phone Number 305-0808 Serial Number: 09/253-628
Mail Box and Bldg/Room Location: CR 11/7416 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Recombinant biologically active human zone
pellucida protein 3 (H2P3) to test male fertility
Inventors (please provide full names): Ke-wen Ding, Sergio Oehninger, William E. Gibbons

Earliest Priority Filing Date: 2/19/98

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please search sequences:
Seq ID NOs 1-4

Point of Contact:
Mona Smith
Technical Info. Specialist
CM1 12C14 Tel: 308-3278

Seq ID No. 1 is being claimed.

See attached claims, data sheet, relevant pages of specification, and drawings.

Thanks,
Lisa C
☺

STAFF USE ONLY		Type of Search	Vendors and cost where applicable
Searcher: <u>SMITH</u>	NA Sequence (#) <u>1</u>	STN <u>4965</u>	
Searcher Phone #: <u>1</u>	AA Sequence (#) <u>1</u>	Dialog	
Searcher Location:	Structure (#)	Questel/Orbit	
Date Searcher Picked Up:	Bibliographic	Dr. Link	
Date Completed: <u>4-28-2000</u>	Litigation	Lexis/Nexis	
Searcher Prep & Review Time: <u>35</u>	Fulltext	Sequence Systems	
Clerical Prep Time:	Patent Family	WWW/Internet	
Online Time: <u>20</u>	Other	Other (specify)	

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MPsrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on:      Fri Apr 28 14:27:17 2000;  MasPar time 3.79 Seconds
              236.177 Million cell updates/sec
Tabular output not generated.

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Title: >US-09-252-828-1
Description: (1-41) from US09252828.dep
Perfect Score: 325
Sequence: 1 SMFVQGADICQCCNCKGDCGTPSHSRRODPHYNSQMSKRSVS 41

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Scoring table: PAM 150
Gap 11

Searched: 188963 seqs, 23686106 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

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Database: a-geneseq36
          1:geneseqP
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Statistics: Mean 23.819; Variance 80.040; scale 0.298

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	301	92.6	223	1	R65552	Cynomolgus Monkey zona	2.30e-22
2	301	92.6	223	1	W81820	M. cynomolgus ZPC Prot	2.30e-22
3	299	92.0	372	1	R22239	Human zp3.	4.00e-23
4	253	77.8	424	1	R53498	Marmoset zp3.	2.9e-13
5	213	65.5	426	1	R55199	Canine zona pellucida	6.81e-13
6	213	65.5	426	1	W81809	Canine ZPC protein.	6.81e-13
7	195	60.0	261	1	R60165	Feline zona pellucida	8.51e-11
8	195	60.0	424	1	R47198	Feline zona pellucida	8.51e-11
9	195	60.0	424	1	R53202	Feline zona pellucida	8.51e-11
10	195	60.0	426	1	W81812	Feline ZPC protein.	8.51e-11
11	195	60.0	424	1	R48068	CZP-3.	8.51e-11
12	172	52.9	224	1	R07058	Mouse zp3 gene product	3.78e-11
13	161	49.5	258	1	R69651	Partial porcine zona p	6.73e-08
14	161	49.5	258	1	R41004	p1g ZPp-3.	6.73e-08
15	161	49.5	420	1	R69950	Porcine zona pellucida	6.73e-08
16	161	49.5	421	1	R55196	Porcine zona pellucida	6.73e-08
17	161	49.5	421	1	W81806	Porcine ZPC protein.	6.73e-08
18	156	48.0	421	1	R55205	Bovine zona pellucida	2.47e-08
19	156	48.0	421	1	W81815	Bovine ZPC protein.	2.47e-08
20	132	40.3	422	1	Y01774	Brushalt possum zp-3	1.16e-08
21	131	40.3	415	1	W81807	Rabbit ZPC protein.	1.49e-08
22	131	40.3	415	1	R55197	Rabbit zona pellucida	1.49e-08
23	121	37.2	16	1	R65671	Human zona pellucida 3	1.83e-04

45	1.36e-04	Tammar wallaby ZP-3 pr	404	1	Y01773	121	37.2	1.36e-04
25	1.03e-03	Zona pellucida protein	15	1	W66123	114	35.1	1.03e-03
24	9.88e+00	zona pellucida protein	10	1	W66126	75	23.1	9.88e+00
26	1.53e+01	Pemphigus vulgaris ant	614	1	W07908	73	22.5	1.53e+01
27	1.53e+01	Human pemphigus vulgar	999	1	R30742	73	22.5	1.53e+01
28	1.91e+00	Caspase activated nucle	338	1	Y04123	72	22.2	1.91e+00
29	2.94e+00	Addition sequence used	21	1	W69478	20	21.5	2.94e+00
30	2.94e+00	Human mature von Wille	70	21.5	2050	170	21.5	2.94e+00
31	5.59e+00	Streptococcus pneumonia	115	1	W62671	32	20.6	5.59e+00
32	5.59e+00	Chicken acetylcholine	512	1	R06263	67	20.6	5.59e+00
33	6.91e+00	Protein encoded by ORF	254	1	W1200	66	20.3	6.91e+00
34	6.91e+00	Chicken adenovirus typ	282	1	R88515	66	20.3	6.91e+00
35	6.91e+00	Kaposi's sarcoma assoc	327	1	R97845	66	20.3	6.91e+00
36	6.91e+00	Kaposi's sarcoma assoc	327	1	R93661	37	19.7	6.91e+00
37	6.91e+00	Human acetyl choline r	457	1	W03631	38	20.3	6.91e+00
38	6.91e+00	Human acetyl choline r	532	1	W07092	39	20.3	6.91e+00
39	6.91e+00	Arbidopsis thaliana g	596	1	W2200	40	20.3	6.91e+00
40	6.91e+00	HSV-2 strain SB5 Cont1	603	1	W2108	66	20.3	6.91e+00
41	8.51e+01	HSV-2 strain SB5 Cont1	259	1	W4125	41	20.0	8.51e+01
42	1.05e+00	GSV/GI transport recep	449	1	R36984	65	20.0	1.05e+00
43	1.05e+00	Acetylcholine receptor	449	1	R86491	64	19.7	1.05e+00
44	1.05e+00	Acetylcholine receptor	449	1	R86491	64	19.7	1.05e+00
45	1.05e+00	Sequence of von Willeb	2813	1	P60053	64	19.7	1.05e+00

ALIGNMENTS

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RESULT      1
ID           1
AC           R66552 standard; Protein; 223 AA.
DE           03-FEB-1995 (first entry)
DE           Cynomolgus monkey zona pellucida ZPC protein.
KW           Cynomolgus Monkey; zona pellucida; ZPC; Immunoreception.
OS           Macaca cynomolgus.
PN           WC0411019-A.
PD           26-MAY-1994.
PF           06-NOV-1993; U10851.
PR           09-NOV-1992; US-973341.
PR           29-JAN-1993; US-012930.
PA           (ZONA-) ZONAGEN INC.
PI           Harris JD, Hsu KT, Podolski JS;
PI           WPI: 94-183156/22.
DR           N-PSDB: 079682.
PT           Use of zona pellucida proteins and antibodies - for inducing
PT           reproducible transient infertility or permanent sterility in
PT           female mammals
PS           Example 12; Page 132-133; 154pp; English.
SC           Cynomolgus monkey cDNA libraries were constructed in lambda gt10
CC           using mRNA isolated from a set of ovaries collected from monkeys
CC           aged 1.5 and 2 years and a second set from monkeys aged 3, 4 and 14
CC           years of age. The libraries were screened with probes encoding
CC           porcine ZPA, ZPB and ZPC proteins. Positive clones were analysed
CC           further by Southern hybridisation using the porcine probes. Clones
CC           encoding Cynomolgus monkey ZPA, ZPB and ZPC proteins were
CC           identified (see Q79680-Q79682). Q79682 is the insert from the
CC           largest partial ZPC clone which contains just over 50% of the
CC           C-terminal portion of the full-length sequence and contains an ORF
CC           of 672bp; R66552 is the amino acid sequence deduced from the ORF.
SQ           Sequence      223 AA;

Query Match          92.6%; Score 301; DB 1; Length 223;
Best Local Similarity 90.2%; Pred. No. 2,30e-25;
Matches      37; Conservative      3; Mismatches      1; Indels      0; Gaps      0

Db      107 SWPVEGPDADICCCCKGDCGTPSHSRORPVYSQMSRSAS 147
      |||:|||||:|||||:|||||:|||||:|||||:|||||:
QY      1 SWPVGPDADICCCCKGDCGTPSHSRORPVYSQMSRSVS 41
      :
      :
      :

RESULT      2
ID           1
AC           W81820 standard; Protein; 223 AA.
DE           29-JAN-1999 (first entry)
DE           M. cynomolgus ZPC protein.
KW           M. cynomolgus ZPC protein.
OS           M. cynomolgus ZPC protein.

```


CC (R55202) from the feline ZPC clone was approximately 70% homologous
CC to canine ZPC protein.
CC
SQ Sequence 424 AA;

Query Match	60.08;	Score 195;	DB 1;	Length 424;
Best Local Similarity	55.08;	Pred. No. 8.51e-13;		
Matches	22;	Conservative	7;	Mismatches 11; Indels 0; Gaps 0;

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Db      307 WEPEVGPADICNCCNKSGCGLGFSRWLSHLDNRWNNKAS 346
      ||||:||||| |||| | :||: ||: | : |
Qy      2 WEPVQGPADICCCNKGGCGTFSHRQRPVMSQWSRSVY 41

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RESULT 10
ID M81812 standard: Protein; 424 AA.
AC M81812;
DT 29-JAN-1999 (first entry)
DE Feline ZPC protein.
KW ZPC; zona pellucida; infertility; sterility; immunocontraceptive;
RV vaccine; feline.
OS Felis sp.
PN US5837497-A.
PD 17-NOV-1998.
PF 07-JUN-1995; 484993.
PR 09-NOV-1993; US-149223.
PR 09-NOV-1992; US-973341.
PR 29-JAN-1993; US-012990.
PR 07-JUN-1995; US-484993.
PA (ZONA-) ZONAGEN INC.
PI Harris JD;
DR WPI; 99-023447/02.
DR N-PSDB; V64794.
PT Isolated zona pellucida DNA from different mammals - used to develop
PT products which can be used for vaccination to induce transient
PT infertility or permanent sterility in female mammals
PS Claim 5; Column 99-102; 84pp; English.
CC This sequence represents a feline ZPC protein isolated from zona
CC pellucida. This protein can be used in a method for specifically
CC inducing transient infertility or permanent sterility in a host
CC animal by selective vaccination with specific zona pellucida proteins
CC or immunocontraceptively active fragments.
SQ Sequence 424 AA;

Query Match	60.0%	Score 195	DB 1	Length 424
Best Local Similarity	55.0%	Pred. No.	8.51e-13	
Matches	22	Conservative	7	Mismatches 11, Indels 0, Gaps 0;
Db	307	WEPVGPADICCNCKGSCGCGQGRSMRLSHDRPMHKMAS	346	
Oy	2	WEPVGPADICCNCKGSCGCGPFSHRSKRPAMVMSQMSVSVS	41	

RESULT	11	
ID	RA8068	standard; Protein; 426 AA.
AC	RA8068;	
DT	03-AUG-1994	(first entry)
DE	CZP-3.	
KE	Canine; dog; contraceptive; CZP; canine zona pellucida;	
KW	transformant; E.coli; clone.	
OS	Canis familiaris.	
PN	J05336974-A.	
PD	21-DEC-1993.	
PF	15-DEC-1992; 353990.	
PR	26-DEC-1991; JP-357671.	
PA	(TOFU) TONEN CORP.	
DR	WPI; 94-051146/07.	
DR	N-PSDB; Q55424.	
PT	Isolated canine zona pellucida CZP-3 -	for use in contraceptive
PT	vaccine	
PS	Claim 2; Page 11; 17pp; Japanese.	
CC	The sequence shows a CZP-3 protein which can be used as a	
CC	preparation for a contraceptive for dogs. The CZP-3 gene is cloned	
CC	using primers (Q55425-26) into E.coli. The resulting transformant	

CC produces the protein.
SQ Sequence 426 AA;

Query Match	60.0%;	Score 195;	DB 1;	Length 426;
Best Local Similarity	59.0%;	Pred. NO. 8.51e-13;		
Matches	23;	Conservative	9;	Mismatches 7;
			Indels	0;
			Gaps	0;

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Db 308 YPVEGSADICRCNKSGSCGLGSRSLHLERGNKRSVS 346
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QY 3 FVQGPADICCCCNKGDCGTPSHSRQPHVMSQNSRSVS 41
```

RESULT 12
ID R07058 standard; protein; 424 AA.
AC R07058;
DT 18-JAN-1991 (first entry)
DE Mouse zfp3 gene product epitopic for Ab which inhibits fertilisation
DE of an oocyte by a sperm in mammalian female.
KW Contraceptive; zfp3 protein; zona pellucida.
OS Mus musculus.
PN US7364379-A.
PD 28-AUG-1990.
PF 12-JUN-1989; 364379.
PR 12-JUN-1989; US-364379.
PA (USSH) NAT INST DIABETES.
PI Jurrien D;
DR WPI: 90-297734/39.
DR N-PDB: 006126.
PT Contraceptive antibody vaccine for mammalian female - comprises
PT peptide epitope of zona pellucida protein, minimises possibility
PT of birth defects if failed contraception.
PS Disclosure; Fig 1; 93pp. English.
CC Vaccine provides long term, non-permanent contraception in mammals,
CC by inhibition of fertilisation rather than abortive methods, thus
CC minimising risk of birth defects.
CC Gene product comprises epitope to zona pellucida protein and vector
CC and transformed expression systems are also claimed.
SQ Sequence 424 AA.

	Query Match	52.9%	Score 172;	DB 1;	Length 424;
	Best Local	Similarity 53.7%;	Pred. No. 3,78e-10;		
	Matches	22;	Conservative	9;	Mismatches 10;
				Indels	0;
				Gaps	0;
Db	309	SWLPEGDADIDCCGCSHGCSNSSGFOFHGRPQWKEKYS	349		
		: : : : : : : :			
0y	1	SWPEVQSPADICCCCKNGDCGTFSRQSHSRQVHWSQMRKSY	41		

ID	RESULT	13
AC	R96951; standard; Protein; 258 AA.	
DT	18-JUL-1996 (first entry)	
DE	Partial porcine zona pellucida 3, PZP-3(258).	
KM	PZP-3; porcine zona pellucida 3; contraceptive vaccine; antigen;	
KM	PZP-3(258); ds.	
OS	Sus scrofa.	
FH	Key	
FT	Location/Qualifiers	
FT	1..258	
FT	/label= "PZP-3(258)	
FT	/note= "corresponds to amino acids 106-363 of PZP-3	
FT	(R96950)."	
PN	J06179698-A.	
PD	28-JUN-1994.	
PF	15-DEC-1992; 353992.	
PR	15-DEC-1992; JP-353992.	
PA	(TOFU) TONEN CORP.	
DR	WPI, 94-245693/30.	
PT	N-PDSB; T14908.	
PT	Pig zona pellucida-3 related peptide(s) - useful as contraceptive	
PT	vaccine antigen	
PS	Example 1: Fig 1: 14pp; Japanese.	
CC	The present sequence is that of recombinant porcine zona pellucida 3	
CC	(PZP-3) 258 (R96951). In the specification it is stated that PZP-3(258)	

CC corresponds to amino acids 106-363 of the full length PZP-3 (R96950).
 CC The PZP-3 gene was isolated from the ovaries of pigs and introduced
 CC into suitable host cells for expression. Recombinant PZP-3(258) is
 CC expressed by pMAL-c-PZP-3(258) in E. coli JM109. Peptides wholly or
 CC partially related to PZP-3, partic. between amino acids 106-363, are
 CC useful as contraceptive vaccine antigens for pigs. See also T14894-908.
 SO Sequence 258 AA.

Query Match 49.5%; Score 161; DB 1; Length 258;
 Best Local Similarity 70.4%; Pred. No. 6,73e-09;
 Matches 19; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 202 WSPVGPAYICRCCHKGCGTSPSLSRK 228
 QY 2 WFPVGPADICCCCKNKGDGCTPSHSRR 28

RESULT 14
 ID R41004 standard; Protein; 258 AA.

AC R41004.
 DT 08-FEB-1994 (first entry)
 DE Pig PZP-3.
 KW Zona pellucida: PZP-3; primer: polymerase chain reaction; PCR;
 KW expression: vaccine; antigen; contraception; sterility; pig.
 OS Sus scrofa.
 PN J05176771-A.
 PD 20-JUL-1993.
 PF 29-NOV-1991; 342318.
 PR 29-NOV-1991; JP-342318.
 PA (TOFU) TONEN CORP.
 DR WPI: 93-260855/33.
 DR N-PSDB: Q48695.
 PT DNA coding pig zona pellucida PZP-3 - prepd. by recombinant DNA
 PT - contg. base sequence coding (part of) partial aminoacid sequence
 of PZP-3 to proper replicable expression vector etc.
 PS Claim 1: Page 6-7; 13pp. Japanese.
 CC The primers given in Q48695-94 are used in the isolation of PZP-3
 CC DNA. Pig zona pellucida PZP-3 is useful as a vaccine antigen for
 CC pig contraception or sterility.
 SO Sequence 258 AA;

Query Match 49.5%; Score 161; DB 1; Length 258;
 Best Local Similarity 70.4%; Pred. No. 6,73e-09;
 Matches 19; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 202 WSPVGPAYICRCCHKGCGTSPSLSRK 228
 QY 2 WFPVGPADICCCCKNKGDGCTPSHSRR 28

RESULT 15
 ID R96950 standard; Protein; 420 AA.
 AC R96950.
 DT 18-JUL-1996 (first entry)
 DE Porcine zona pellucida 3 (PZP-3).
 KW PZP-3; porcine zona pellucida 3; contraceptive vaccine; antigen;
 KW PZP-3(258).
 OS Sus scrofa.
 PN J06179698-A.
 PD 28-JUN-1994.
 PF 15-DEC-1992; 353992.
 PR 15-DEC-1992; JP-353992.
 PA (TOFU) TONEN CORP.
 DR WPI: 94-245693/30.
 DR N-PSDB: T14894.
 PT Pig zona pellucida-3 related peptide(s) - useful as contraceptive
 PT vaccine antigen
 PS Claim 1: Page 9-10; 14pp. Japanese.
 CC The present sequence is that of porcine zona pellucida 3 (PZP-3). The
 CC PZP-3 gene (T14894) was isolated from the ovaries of pigs and introduced
 CC into suitable host cells for expression. Peptides wholly or partially
 CC related to PZP-3, partic. between amino acids 106-363 (See R96951), are
 CC useful as contraceptive vaccine antigens for pigs. See also T14895-908.

SO Sequence 420 AA;

Query Match 49.5%; Score 161; DB 1; Length 420;
 Best Local Similarity 70.4%; Pred. No. 6,73e-09;
 Matches 19; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 307 WSPVGPAYICRCCHKGCGTSPSLSRK 333
 QY 2 WFPVGPADICCCCKNKGDGCTPSHSRR 28

Search completed: Fri Apr 28 14:27:50 2000
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WORLDWIDE
(TM)

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MSrch_pp protein - protein database search, using Smith-Waterman algorithm
Run on: Fri Apr 28 14:28:08 2000; MasPar time 2.38 Seconds
Tabular output not generated. 223.353 Million cell updates/sec

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Description: (1-41) from US09252828.pep
Perfect Score: 325
Sequence: 1 SMFPVQGPADICCCCKGDCGTPSHSRQPHVMSQMSRSVS 41

Scoring table: PAM 150
Gap 11

Searched: 131253 seqs, 12956647 residues

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database: a-issued

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Statistics: Mean 22.706; Variance 81.406; scale 0.279

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
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2	314	96.6	424	1	US-08-038-	Sequence 4, Applicatio	1.37e-25
3	314	96.6	424	1	US-08-453-	Sequence 7, Applicatio	1.37e-25
4	314	96.6	424	2	US-08-484-	Sequence 61, Applicati	1.37e-25
5	314	96.6	424	2	US-08-862-	Sequence 7, Applicatio	1.37e-25
6	301	92.6	223	2	US-08-484-	Sequence 49, Applicati	4.11e-24
7	301	92.6	223	2	US-08-484-	Sequence 49, Applicati	4.11e-24
8	301	92.6	223	2	US-08-484-	Sequence 49, Applicati	4.11e-24
9	301	92.6	223	2	US-08-480-	Sequence 49, Applicati	4.11e-24
10	301	92.6	223	2	US-08-480-	Sequence 49, Applicati	4.11e-24
11	213	65.5	426	2	US-08-484-	Sequence 12, Applicati	3.05e-14
12	213	65.5	426	2	US-08-484-	Sequence 12, Applicati	3.05e-14
13	213	65.5	426	2	US-08-484-	Sequence 12, Applicati	3.05e-14
14	213	65.5	426	2	US-08-484-	Sequence 12, Applicati	3.05e-14
15	195	60.0	424	2	US-08-480-	Sequence 18, Applicati	2.92e-12
16	195	60.0	424	2	US-08-480-	Sequence 18, Applicati	2.92e-12
17	195	60.0	424	2	US-08-484-	Sequence 18, Applicati	2.92e-12
18	195	60.0	424	2	US-08-484-	Sequence 18, Applicati	2.92e-12
19	172	52.9	424	1	US-08-038-	Sequence 8, Applicatio	9.25e-10
20	172	52.9	424	1	US-08-038-	Sequence 8, Applicatio	9.25e-10
21	172	52.9	424	1	US-08-038-	Sequence 8, Applicatio	9.25e-10
22	172	52.9	424	1	US-08-038-	Sequence 8, Applicatio	9.25e-10
23	161	49.5	421	2	US-08-484-	Sequence 6, Applicatio	1.41e-08

24	161	49.5	421	2	US-08-480-	Sequence 6, Applicatio	1.41e-08
25	161	49.5	421	2	US-08-484-	Sequence 6, Applicatio	1.41e-08
26	161	49.5	421	2	US-08-484-	Sequence 6, Applicatio	1.41e-08
27	156	48.0	421	2	US-08-484-	Sequence 24, Applicati	4.82e-08
28	156	48.0	421	2	US-08-484-	Sequence 24, Applicati	4.82e-08
29	156	48.0	421	2	US-08-484-	Sequence 24, Applicati	4.82e-08
30	156	48.0	421	2	US-08-480-	Sequence 24, Applicati	4.82e-08
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37	121	37.2	16	1	US-08-453-	Sequence 11, Applicati	2.25e-04
38	121	37.2	16	2	US-08-862-	Sequence 10, Applicati	2.25e-04
39	70	21.5	21	2	US-08-754-	Sequence 10, Applicati	2.08e+01
40	67	20.6	457	1	US-08-278-	Sequence 3, Applicatio	3.86e+01
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42	66	20.3	327	3	PCT-US95-1	Sequence 35, Applicati	4.73e+01
43	64	19.7	54	2	US-08-691-	Sequence 42, Applicati	7.09e+01
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ALIGNMENTS

RESULT 1 STANDARD: PRT: 424 AA.

US-08-453-472-7

xxxxxx

Sequence 7, Application US/08453472

Sequence 7, Application US/08453472

Patent No. 5626846

GENERAL INFORMATION:

APPLICANT: DEAN, JURRIEN

TITLE OF INVENTION: CONTRACEPTIVE VACCINE

TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: MORGAN & FINNEGAN

STREET: 345 PARK AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10154

COMPUTER READABLE FORM:

MEDIUM TYPE: FLOPPY DISK

COMPUTER: IBM PC COMPATIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WORDPERFECT 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/453,472

FILING DATE: 30-May-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/038,948

FILING DATE: 26-MAR-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/930,462

FILING DATE: 20-AUG-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/364,379

FILING DATE: 12-JUN-1989

ATTORNEY/AGENT INFORMATION:

NAME: DOROTHY R. AUTH

REGISTRATION NUMBER: 36,434

REFERENCE/DOCKET NUMBER: 2026-4032 US3

TELECOMMUNICATION INFORMATION:

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CC      FILING DATE: 12-JUN-1989
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: SCOTT, Watson T.
CC      REGISTRATION NUMBER: 26,581
CC      REFERENCE/DOCKET NUMBER: 99152/E-266-88/2
CC      TELECOMMUNICATION INFORMATION:
CC      TELEPHONE: (202) 861-3000
CC      TELEFAX: (202) 822-0944
CC      TELEX: 6714627 CUSH
CC      INFORMATION FOR SEQ ID NO: 4:
CC      SEQUENCE CHARACTERISTICS:
CC      LENGTH: 424 amino acids
CC      TYPE: amino acid
CC      STRANDEDNESS: single
CC      TOPOLOGY: linear
CC      MOLECULE TYPE: protein
CC      SEQUENCE 424 AA; 47028 MW; 954880 CN;
SQ
CC
CC      Query Match          96.6%; Score 314; DB 1; Length 424;
CC      Best Local Similarity 95.1%; Pred.No.1.37e-25;
CC      Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0.
CC
D6      308 SWFPEYGPADICCCCNKGDCCTPSHSRRQPHVMSQMSRSAS 348
Q7      1 SWFVQGPADICCCCNKGDCCTPSHSRRQPHVMSQMSRSYSV 41
CC
RESULT      3
ID      US-08-453-952-7      STANDARD;      PRT;      424 AA.
XX      xxxxxx
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XX      Sequence 7, Application US/08453952
DE      Sequence 7, Application US/08453952
CC      Patent No. 5672488
CC      GENERAL INFORMATION:
CC      APPLICANT: DEAN, JURRIEN
CC      TITLE OF INVENTION: CONTRACEPTIVE VACCINE
CC      TITLE OF INVENTION: BASED ON ALLOIMUNIZATION WITH ZONA PELLUCIDA
CC      TITLE OF INVENTION: POLYPEPTIDES
CC      NUMBER OF SEQUENCES: 12
CC      CORRESPONDENCE ADDRESS:
CC      ADDRESSEE: MORGAN & FINNEGAN
CC      STREET: 345 PARK AVENUE
CC      CITY: NEW YORK
CC      STATE: NEW YORK
CC      COUNTRY: USA
CC      ZIP: 10154
CC      COMPUTER READABLE FORM:
CC      MEDIUM TYPE: FLOPPY DISK
CC      COMPUTER: IBM PC COMPATIBLE
CC      OPERATING SYSTEM: PC-DOS/MS-DOS
CC      SOFTWARE: WORDPERFECT 5.1
CC      CURRENT APPLICATION DATA:
CC      APPLICATION NUMBER: US/08/453,952
CC      FILING DATE: 30-May-1995
CC      CLASSIFICATION: 424
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 08/038,948
CC      FILING DATE: 26-MAR-1993
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/930,462
CC      FILING DATE: 20-AUG-1992
CC      PRIOR APPLICATION DATA:
CC      APPLICATION NUMBER: US 07/364,379
CC      FILING DATE: 12-JUN-1989
CC      ATTORNEY/AGENT INFORMATION:
CC      NAME: DOROTHY R. AUTH
CC      REGISTRATION NUMBER: 36,434
CC      REFERENCE/DOCKET NUMBER: 2026-4032 US4

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CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: (212) 758-4800
CC TELEFAX: (212) 751-6849
CC TELEX: 421792
CC INFORMATION FOR SEQ ID NO: 7:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 424
CC TYPE: amino acid
CC STRANDEDNESS: single
CC TOPOLOGY: unknown
CC MOLECULE TYPE: protein
CC ORIGINAL SOURCE:
CC ORGANISM: human
CC STRAIN:
CC INDIVIDUAL ISOLATE:
CC DEVELOPMENTAL STAGE:
CC HAPLOTYPE:
CC TISSUE TYPE:
CC CELL TYPE:
CC CELL LINE:
CC ORGANELLE:
CC FEATURE:
CC NAME/KEY: ZP3
CC LOCATION:
CC IDENTIFICATION METHOD:
CC OTHER INFORMATION: human ZP3 protein
CC SEQUENCE 424 AA; 47028 MW; 954880 CN;
SQ
Query Match 96.6%; Score 314; DB 1; Length 424;
Best Local Similarity 95.1%; Pred. No. 1.37e-25;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 308 SWPVEGPADICCCCKNGDCGTPSHSRQPHYMSQMSRSAS 348
QY 1 SWPVEGPADICCCCKNGDCGTPSHSRQPHYMSQMSRSVS 41
RESULT 4
ID US-08-484-158B-61 STANDARD: PRT; 424 AA.
XX xxxxxx
AC
DT
DE Sequence 61, Application US/08484158B
XX
CC Sequence 61, Application US/08484158B
CC Patent No. 5976545
CC GENERAL INFORMATION:
CC APPLICANT: Harris Ph.D., Jeffrey D.
CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Pharmaceutical Compositions for
CC TITLE OF INVENTION: Immuncontraception
CC NUMBER OF SEQUENCES: 61
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
CC ADDRESSEE: Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,158B
CC FILING DATE: 07-JUNE-95
CC CLASSIFICATION: 514
CC PRIOR APPLICATION DATA:

CC APPLICATION NUMBER: 08/149,223
CC FILING DATE: 09-NOV-93
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-93
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-92
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 32794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 61:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 424 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC DESCRIPTION: /desc =
CC DESCRIPTION: "deduced amino acid sequence of human ZPC"
CC SEQUENCE 424 AA; 47028 MW; 954880 CN;
SQ
Query Match 96.6%; Score 314; DB 2; Length 424;
Best Local Similarity 95.1%; Pred. No. 1.37e-25;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
DB 308 SWPVEGPADICCCCKNGDCGTPSHSRQPHYMSQMSRSAS 348
QY 1 SWPVEGPADICCCCKNGDCGTPSHSRQPHYMSQMSRSVS 41
RESULT 5
ID US-08-862-903-7 STANDARD: PRT; 424 AA.
XX xxxxxx
AC
DT
DE Sequence 7, Application US/08862903
XX
CC Sequence 7, Application US/08862903
CC Patent No. 5916768
CC GENERAL INFORMATION:
CC APPLICANT: DEAN, JURRIEN
CC TITLE OF INVENTION: CONTRACEPTIVE VACCINE
CC TITLE OF INVENTION: BASED ON ALLOIMMUNIZATION WITH ZONA PELLUCIDA
CC NUMBER OF SEQUENCES: 12
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: MORGAN & FINNEGAN
CC STREET: 345 PARK AVENUE
CC CITY: NEW YORK
CC STATE: NEW YORK
CC COUNTRY: USA
CC ZIP: 10154
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: FLOPPY DISK
CC COMPUTER: IBM PC COMPATIBLE
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: WORDPERFECT 5.1
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/862,903
CC FILING DATE: 30-MAY-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/038,948
CC FILING DATE: 26-MAR-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 07/930,462

CC FILING DATE: 20-AUG-1992
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: US 07/364,379
 CC FILING DATE: 12-JUN-1989
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: DOROTHY R. AUTH
 CC REGISTRATION NUMBER: 36,434
 CC REFERENCE/DOCKET NUMBER: 2026-4032 US4
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: (212) 758-4800
 CC TELEFAX: (212) 751-6849
 CC INFORMATION FOR SEQ ID NO: 7:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 424
 CC TYPE: amino acid
 CC STRANDEDNESS: single
 CC TOPOLOGY: unknown
 CC MOLECULE TYPE: protein
 CC ORIGINAL SOURCE:
 CC ORGANISM: human
 CC STRAIN:
 CC INDIVIDUAL ISOLATE:
 CC DEVELOPMENTAL STAGE:
 CC HARLOT TYPE:
 CC TISSUE TYPE:
 CC CELL LINE:
 CC ORGANELLE:
 CC FEATURE:
 CC NAME/KEY: ZP3
 CC LOCATION:
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 CC OTHER INFORMATION: human ZP3 protein
 CC SEQUENCE 424 AA; 47028 MW; 954880 CN;
 CC
 CC Query Match 96.6%; Score 314; DB 2; Length 424;
 CC Best Local Similarity 95.1%; Pred. No. 1.37e-25;
 CC Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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 CC Db 308 SWFVPGADICCCCNKGDCTPSHSRQPHVMSQMSRSAS 348
 CC 1 SWFVPGADICCCCNKGDCTPSHSRQPHVMSQMSRSAS 41
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 CC RESULT 6
 CC ID US-08-484-993B-49 STANDARD; PRT; 223 AA.
 CC XX
 CC xxxxxx
 CC
 CC Sequence 49, Application US/08484993B
 CC Patent No. 5837497
 CC GENERAL INFORMATION:
 CC APPLICANT: Harris Ph.D., Jeffrey D.
 CC APPLICANT: Hsu, Kuang T.
 CC APPLICANT: Podolski, Joseph S.
 CC TITLE OF INVENTION: Materials and Methods for Immunocontraception
 CC NUMBER OF SEQUENCES: 59
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 CC STREET: 6300 Sears Tower, 233 South Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: United States of America
 CC ZIP: 60606-6402
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS

CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/484,993B
 CC FILING DATE: 09-NOV-1993
 CC CLASSIFICATION: 424
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/012,990
 CC FILING DATE: 29-JAN-1993
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 07/973,341
 CC FILING DATE: 09-NOV-1992
 CC ATTORNEY/AGENT INFORMATION:
 CC NAME: Clough, David W.
 CC REGISTRATION NUMBER: 36,107
 CC REFERENCE/DOCKET NUMBER: 31745
 CC TELECOMMUNICATION INFORMATION:
 CC TELEPHONE: 312/474-6653
 CC TELEFAX: 312/474-0448
 CC TELETYPE: 25-3856
 CC INFORMATION FOR SEQ ID NO: 49:
 CC SEQUENCE CHARACTERISTICS:
 CC LENGTH: 223 amino acids
 CC TYPE: amino acid
 CC TOPOLOGY: linear
 CC MOLECULE TYPE: protein
 CC SEQUENCE 223 AA; 24553 MW; 26656 CN;
 CC
 CC Query Match 92.6%; Score 301; DB 2; Length 223;
 CC Best Local Similarity 90.2%; Pred. No. 4.11e-24;
 CC Matches 37; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 CC
 CC Db 107 SWFVPGADICCCCNKGDCTPSHSRQPHVMSQMSRSAS 147
 CC 1 SWFVPGADICCCCNKGDCTPSHSRQPHVMSQMSRSAS 41
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 CC RESULT 7
 CC ID US-08-484-158B-49 STANDARD; PRT; 223 AA.
 CC XX
 CC xxxxxx
 CC
 CC Sequence 49, Application US/08484158B
 CC Patent No. 5976545
 CC GENERAL INFORMATION:
 CC APPLICANT: Harris Ph.D., Jeffrey D.
 CC APPLICANT: Hsu, Kuang T.
 CC APPLICANT: Podolski, Joseph S.
 CC TITLE OF INVENTION: Pharmaceutical Compositions for
 CC NUMBER OF SEQUENCES: 61
 CC CORRESPONDENCE ADDRESS:
 CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
 CC STREET: 6300 Sears Tower, 233 South Wacker Drive
 CC CITY: Chicago
 CC STATE: Illinois
 CC COUNTRY: United States of America
 CC ZIP: 60606-6402
 CC COMPUTER READABLE FORM:
 CC MEDIUM TYPE: floppy disk
 CC COMPUTER: IBM PC compatible
 CC OPERATING SYSTEM: PC-DOS/MS-DOS
 CC SOFTWARE: Patent Release #1.0, Version #1.25
 CC CURRENT APPLICATION DATA:
 CC APPLICATION NUMBER: US/08/484,158B
 CC FILING DATE: 07-JUNE-95
 CC CLASSIFICATION: 514
 CC PRIOR APPLICATION DATA:
 CC APPLICATION NUMBER: 08/149,223

CC FILING DATE: 09-NOV-93
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-93
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-92
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 32794
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 49:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 223 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 223 AA: 24553 MW: 26656 CN;
SQ
DB 107 SWFPPVGPADICCCCKGDCGTPSHSRPHVMSQMSRSAS 147
Y 1 SWFPPVGPADICCCCKGDCGTPSHSRPHVMSQMSRSVS 41
RESULT 8
ID -US-08-484-596A-49 STANDARD: PRT: 223 AA.
AC xxxxxx
XX
XX
XX
DE Sequence 49, Application US/08484596A
CC Sequence 49, Application US/08484596A
CC Patent No. 5961228
CC GENERAL INFORMATION:
CC APPLICANT: Harris Ph.D., Jeffrey D.
CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Materials and Methods for Immunoccontraception
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,596A
CC FILING DATE:
CC FILING DATE: 09-NOV-1992
CC CLASSIFICATION:
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 08/149,223
CC FILING DATE: 11-NOV-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.

CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 31745
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 49:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 223 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 223 AA: 24553 MW: 26656 CN;
SQ
DB 107 SWFPPVGPADICCCCKGDCGTPSHSRPHVMSQMSRSAS 147
Y 1 SWFPPVGPADICCCCKGDCGTPSHSRPHVMSQMSRSVS 41
RESULT 9
ID US-08-480-150A-49 STANDARD: PRT: 223 AA.
AC xxxxxx
XX
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DE Sequence 49, Application US/08480150A
CC Sequence 49, Application US/08480150A
CC Patent No. 5989550
CC GENERAL INFORMATION:
CC APPLICANT: Harris Ph.D., Jeffrey D.
CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Materials and Methods for Immunoccontraception
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patentin Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,150A
CC FILING DATE:
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149,223
CC FILING DATE: 09-NOV-1993
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-1993
CC PRIOR APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 31745
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 49:

CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 223 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
SQ SEQUENCE 223 AA: 24553 MW: 266656 CN:

Query Match 92.6%; Score 301; DB 2; Length 223;
Best Local Similarity 90.2%; Pred. No. 4,11e-24;
Matches 37; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Db 107 SWPVGADICCCCKGCGTSPSHSRPHVWSOWSRVS 147
QY 1 SWPVGADICCCCKGCGTSPSHSRPHVWSOWSRVS 41

RESULT 10
ID US-08-484-596A-12 STANDARD; PRT; 426 AA.
AC xxxxxx
DT
DE

Sequence 12, Application US/08484596A

Patent No. 5981228

GENERAL INFORMATION:

APPLICANT: Harris Ph.D., Jeffrey D.

APPLICANT: Hsu, Kuang T.

APPLICANT: Podolski, Joseph S.

TITLE OF INVENTION: Materials and Methods for Immunocotraception

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

City: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/484,596A

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/149,223

FILING DATE: 11-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,341

FILING DATE: 09-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 31745

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-0448

TELEFAX: 312/474-6653

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 426 AA: 47367 MW: 972293 CN:

Query Match 65.5%; Score 213; DB 2; Length 426;

Best Local Similarity 60.0%; Pred. No. 3.05e-14;

Matches 24; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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Matches 24; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 307 WYPVGSADICCCCKGCGTSPSHSRPHVWSOWSRVS 346
QY 2 WYPVGSADICCCCKGCGTSPSHSRPHVWSOWSRVS 41

RESULT 11
ID US-08-480-150A-12 STANDARD; PRT; 426 AA.
AC xxxxxx
DT
DE

Sequence 12, Application US/08480150A

Patent No. 5989550

GENERAL INFORMATION:

APPLICANT: Harris Ph.D., Jeffrey D.

APPLICANT: Hsu, Kuang T.

APPLICANT: Podolski, Joseph S.

TITLE OF INVENTION: Materials and Methods for Immunocotraception

NUMBER OF SEQUENCES: 59

CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 6300 Sears Tower, 233 South Wacker Drive

City: Chicago

STATE: Illinois

COUNTRY: United States of America

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,150A

FILING DATE: 07-JUN-1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/149,223

FILING DATE: 09-NOV-1993

APPLICATION NUMBER: 08/012,990

FILING DATE: 29-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/973,341

FILING DATE: 09-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: Clough, David W.

REGISTRATION NUMBER: 36,107

REFERENCE/DOCKET NUMBER: 31745

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312/474-6653

TELEFAX: 312/474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 12:

SEQUENCE CHARACTERISTICS:

LENGTH: 426 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE 426 AA: 47367 MW: 972293 CN:

Query Match 65.5%; Score 213; DB 2; Length 426;

Best Local Similarity 60.0%; Pred. No. 3.05e-14;

Matches 24; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 307 WYPVGSADICCCCKGCGTSPSHSRPHVWSOWSRVS 346

QY 2 WYPVGSADICCCCKGCGTSPSHSRPHVWSOWSRVS 41

CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Materials and Methods for Immunocontraception
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois
CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/484,993B
CC FILING DATE: 09-NOV-1993
CC CLASSIFICATION: 424
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-1993
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 31745
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 18:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 424 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 424 AA; 46853 MW; 929900 CN;
DB 307 WFPVGPADICCCNKGDCGTPSHSRQPHVMSQWSRSVS 41
QY 2 WFPVGPADICCCNKGDCGTPSHSRQPHVMSQWSRSVS 41
Query Match 60.0%; Score 195; DB 2; Length 424;
Best Local Similarity 55.0%; Pred. No. 2.92e-12;
Matches 22; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
RESULT 15
ID US-08-480-150A-18 STANDARD; PRT; 424 AA.
AC xxxxxx
XX
DT
XX
DE Sequence 18, Application US/08480150A
CC Sequence 18, Application US/08480150A
CC Patent No. 5989550
CC GENERAL INFORMATION:
CC APPLICANT: Harris Ph.D., Jeffrey D.
CC APPLICANT: Hsu, Kuang T.
CC APPLICANT: Podolski, Joseph S.
CC TITLE OF INVENTION: Materials and Methods for Immunocontraception
CC NUMBER OF SEQUENCES: 59
CC CORRESPONDENCE ADDRESS:
CC ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
CC STREET: 6300 Sears Tower, 233 South Wacker Drive
CC CITY: Chicago
CC STATE: Illinois

CC COUNTRY: United States of America
CC ZIP: 60606-6402
CC COMPUTER READABLE FORM:
CC MEDIUM TYPE: Floppy disk
CC COMPUTER: IBM PC compatible
CC OPERATING SYSTEM: PC-DOS/MS-DOS
CC SOFTWARE: Patent In Release #1.0, Version #1.25
CC CURRENT APPLICATION DATA:
CC APPLICATION NUMBER: US/08/480,150A
CC FILING DATE: 07-JUN-1995
CC CLASSIFICATION: 424
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: US 08/149,223
CC FILING DATE: 09-NOV-1993
CC APPLICATION NUMBER: 08/012,990
CC FILING DATE: 29-JAN-1993
CC PRIORITY APPLICATION DATA:
CC APPLICATION NUMBER: 07/973,341
CC FILING DATE: 09-NOV-1992
CC ATTORNEY/AGENT INFORMATION:
CC NAME: Clough, David W.
CC REGISTRATION NUMBER: 36,107
CC REFERENCE/DOCKET NUMBER: 31745
CC TELECOMMUNICATION INFORMATION:
CC TELEPHONE: 312/474-6653
CC TELEFAX: 312/474-0448
CC TELEX: 25-3856
CC INFORMATION FOR SEQ ID NO: 18:
CC SEQUENCE CHARACTERISTICS:
CC LENGTH: 424 amino acids
CC TYPE: amino acid
CC TOPOLOGY: linear
CC MOLECULE TYPE: protein
CC SEQUENCE 424 AA; 46853 MW; 929900 CN;
DB 307 WFPVGPADICCCNKGDCGTPSHSRQPHVMSQWSRSVS 41
QY 2 WFPVGPADICCCNKGDCGTPSHSRQPHVMSQWSRSVS 41
Query Match 60.0%; Score 195; DB 2; Length 424;
Best Local Similarity 55.0%; Pred. No. 2.92e-12;
Matches 22; Conservative 7; Mismatches 11; Indels 0; Gaps 0;
Search completed: Fri Apr 28 14:28:28 2000
Job time: 20 secs.

Release 3.1A John F. Collins, Biocomputing Research Unit
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```

Title: >US-09-252-828-1
Description: (1-41) from US09252828..rep
Perfect Score: 325
Sequence: 1 SMFVVGSPADICQCCCKNKDCGPHSRPRPHWMSQMSRSYS 411

```

Searched: 142080 seqs, 47172406 residues

Post-processing: Minimum Match 0%
Listing first 45

Database: pir62

Statistics: Mean 31.323; Variance 49.714; scale 0.630

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description	Pred. No
---------------	-------	----------------	--------	----	-------------	----------

1	314	96.6	424	1	A36000	sperm-binding glycopr	3.56e-55
2	287	88.3	210	2	A56844	POM-ZP3 protein - hum	1.63e-38
3	213	65.5	426	2	S70396	zona pellucida glycop	1.13e-30
4	197	60.6	422	1	A60503	sperm-binding glycopr	6.33e-37
5	195	60.0	424	2	S70393	zona pellucida glycop	1.85e-26
6	172	52.9	424	1	A30334	sperm-binding glycopr	3.54e-21
7	161	49.5	421	1	S70433	zona pellucida glycop	1.07e-18
8	156	48.0	421	1	S70402	zona pellucida glycop	1.39e-17
9	131	40.3	415	2	S70401	zona pellucida glycop	3.81e-12
10	129	39.7	44	2	B44365	sperm receptor ligand	1.01e-11
11	82	25.2	428	1	S52845	ZP3 protein - goldfis	1.80e-02
12	81	24.9	58	2	S52573	zona pellucida glycop	2.71e-02
13	81	24.9	422	2	S52848	egg membrane protein	2.71e-02
14	80	24.6	388	2	S52716	sperm receptor zp3 -	4.06e-02
15	80	24.6	424	2	S52847	egg membrane protein	4.06e-02
16	74	22.8	74	2	A60518	acanthophin d - death	4.32e-01
17	74	22.8	499	2	A28937	triacylglycerol lipas	4.32e-01
18	73	22.5	999	1	IGHU3	desmoglein 3 precursor	6.34e-01
19	72	22.2	65	2	S16019	neurotoxin 6 - indian	9.27e-01
20	72	22.2	71	1	NNN15	long neurotoxin 1 - m	9.27e-01
21	72	22.2	745	2	C70848	probable lcd2 protein	9.27e-01
22	71	21.8	583	2	S19476	hypothetical protein	1.35e+00
23	70	21.5	91	2	G15162	probable ferritinon 1	1.96e+00

45	67	20.6	819	2	C71544	leucine--tRNA ligase	5.89e+00
44	67	20.6	513	1	ACCHD1	nicotinic acetylcholi	5.89e+00
44	67	20.6	357	2	ACCHD1	ig alpha chain C regi	5.89e+00
43	67	20.6	357	1	ACCHD1	ig alpha chain C regi	5.89e+00
42	67	20.6	351	2	C72508	hypothetical protein	5.89e+00
41	67	20.6	343	3	SO9272	ig alpha chain C regi	5.89e+00
40	67	20.6	102	2	T14958	hypothetical protein	5.89e+00
39	68	20.9	641	2	A45054	probable intercellula	4.10e+00
38	68	20.9	267	1	JM0724	interleukin-1 beta pr	4.10e+00
37	68	20.9	224	2	B72699	hypothetical protein	4.10e+00
36	69	21.2	1339	1	A55301	1,3-beta-D-glucan-bi	2.84e+00
35	69	21.2	457	1	ACB0A1	nicotinic acetylcholi	2.84e+00
34	69	21.2	376	2	T09578	nuclear protein Uchl1	2.84e+00
33	69	21.2	147	2	S49526	protein kinase homolo	2.84e+00
33	69	21.2	127	2	T08097	osmorin - sweet orang	2.84e+00
32	69	21.2	118	2	SS4302	hypothetical 13.2X pr	2.84e+00
31	69	21.2	118	2	SS4302	hypothetical 13.2X pr	2.84e+00
30	69	21.5	647	2	JEO337	frizzled-1 protein -	1.96e+00
29	70	21.5	591	2	A40684	early B-cell factor -	1.96e+00
28	70	21.5	570	2	S55059	transcription factor	1.96e+00
27	70	21.5	317	2	H70566	hypothetical protein	1.96e+00
26	70	21.5	218	2	E30542	hypothetical protein	1.96e+00
25	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
24	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
23	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
22	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
21	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
20	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
19	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
18	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
17	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
16	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
15	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
14	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
13	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
12	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
11	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
10	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
9	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
8	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
7	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
6	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
5	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
4	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
3	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
2	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00
1	70	21.5	202	2	A33116	p21 protein - soybean	1.96e+00

ALIGNMENTS

ENTRY	1
TITLE	A36000 #type complete
ALTERNATE_NAMES	spem-binding glycoprotein zp3 precursor - human
ORGANISM	spem receptor Zp3; zona pellucida glycoprotein zp3
DATE	#format_name Homo sapiens #common_name man
	10-Sep-1999 #sequence_revision 10-Sep-1999 #text_ch

ACCESSIONS
REFERENCE

A36000; A44365
A36000

Journal

Chamberlin, M.E.; Dean, J.
Proc. Natl. Acad. Sci. U.S.A. (1990) 87:6014-6018
Human homolog of the mouse sperm receptor.

#access

A36000

```
##re
##cr
```

1-424 ##label CHA
 GB:M60504; GB:M35109; NID:g340491; PIDN:AAA61336.1;
 PID:g340492

#author

van Duin, M.; Polman, J.E.; Verkoelen, C.C.; Bunschoten, H.; Meyerink, J.H.; Olijve, W.; Aitken, R.J.

#title

ligand 2P3: evidence for a second polymorphic allele with a different frequency in the Caucasian and Japanese populations.

```
#access
##st
```

preliminary

```
##Te
##ex
```

329-370, 'S', 372-424 #Label VANT
ntal_source ovary

##no

sequence inconsistent with the nucleotide translation sequence extracted from NCBI backbone (NCBIN:122391, NCBIP:122392)

ceptor for sperm binding. It has O-linked as well as N-linkedbohydrate.

```
#gene
##cr
```

GDB: ZP3A
References GDB: 128007; OMIM: 182889

CLASSIFICA

#superfamily sperm-binding glycoprotein ZP3; ZP domain homology

FEATURE

glycoprotein; oocyte; receptor; sulfoprotein; transmembrane protein

```

1-22      23-424      #domain signal sequence #status predicted #label SIG\
SUMMARY    45-301      #product sperm-binding glycoprotein ZP3 #status
              #domain ZP domain homology #label ZPH
              #length 424 #molecular-weight 47028 #checksum 5505

Query Match
Best Local Similarity 95.1%; Pred. No. 3,56e-55;
Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 SWFVPGADICCCCKGDCGTPSHSRPHVMSOMSRVS 348
QY 1 SWFVPGADICCCCKGDCGTPSHSRPHVMSOMSRVS 41

RESULT 2
ENTRY    A56844      #type complete
TITLE    POM-ZP3 protein - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change
          17-Mar-1999

ACCESSIONS
REFERENCE #authors Kipierstok, S.; Osawa, G.A.; Liang, L.; Modi, W.S.; Dean, J.
           #journal Genomics (1995) 25:354-359
           #title POM-ZP3, a bipartite transcript derived from human ZP3 and a
           #cross-references MUID:95309900.
           #accession A56844
           ##status preliminary
           ##molecule_type mRNA
           ##residues 1-210 ##label KIP
           ##cross-references GB:U10099; NID:9607803; PID:9607804
           #length 210 #molecular-weight 23196 #checksum 5951

Query Match
Best Local Similarity 88.3%; Score 287; DB 1; Length 210;
Matches 36; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Db 146 SWFVPGADICCCCKGDCGTPSHSRPHVMSOMSRVS 186
QY 1 SWFVPGADICCCCKGDCGTPSHSRPHVMSOMSRVS 41

RESULT 3
ENTRY    S70396      #type complete
TITLE    zona pellucida glycoprotein C - dog
ORGANISM #formal_name Canis lupus familiaris #common_name dog
DATE     28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change
          20-Aug-1999

ACCESSIONS
REFERENCE #authors Harris, J.D.; Hibler, D.W.; Fontenot, G.K.; Hsu, K.T.;
           #journal Yurewicz, E.C.; Sacco, A.G.
           #title DNA Seg. (1994) 4:361-393
           #cross-references EMBL:005780; NID:9458276; PID:AAA74387.1;
           #cross-references MUID:95143578
           #accession S70396
           ##status preliminary
           ##molecule_type mRNA
           ##residues 1-426 ##label HAR
           #cross-references EMBL:005780; NID:9458276; PID:AAA74387.1;
           #cross-references MUID:95143578
           #length 426 #molecular-weight 47367 #checksum 16286

CLASSIFICATION
FEATURE 43-299      #domain ZP domain homology #label ZPH
SUMMARY    #length 426 #molecular-weight 47367 #checksum 16286

Query Match
Best Local Similarity 65.5%; Score 213; DB 2; Length 426;
Matches 60; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Matches 24; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

Db 307 WFFVGSADICRCCKGSGCLPGRSRLSLERGMKRSVS 346
QY 2 WFFVGSADICRCCKGSGCLPGRSRLSLERGMKRSVS 41

RESULT 4
ENTRY    A60503      #type complete
TITLE    sperm-binding glycoprotein ZP3 precursor - golden hamster
ALTERNATE_NAMES #formal_name Mesocricetus auratus #common_name golden hamster
ORGANISM #formal_name Mesocricetus auratus #common_name golden hamster
DATE     10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change
          10-Sep-1999

ACCESSIONS
REFERENCE #authors Kinloch, R.A.; Ruiz-Seiler, B.; Massarman, P.M.
           #journal Dev. Biol. (1990) 142:414-421
           #title genomic organization and polypeptide primary structure of
           #cross-references MUID:91078540
           #accession A60503
           ##molecule_type DNA
           ##residues 1-422 ##label KIN
           #cross-references GB:M63629
           #note the authors translated the codon CAA for residue 251 as
           Glu, and AGG for residue 303 as Lys
           This sulfated glycoprotein in the zona pellucida of the oocyte is a
           receptor for sperm binding. It has O-linked as well as N-linked
           carbohydrate.

CLASSIFICATION
FEATURE 45-300      #superfamily sperm-binding glycoprotein ZP3; ZP domain
SUMMARY    #length 422 #molecular-weight 45801 #checksum 6117

Query Match
Best Local Similarity 60.6%; Score 197; DB 1; Length 422;
Matches 23; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

Db 307 SMSVPGDAEYCCGCGSSGSSRSRYAHGVSWPKRSVS 347
QY 1 SMSVPGDAEYCCGCGSSGSSRSRYAHGVSWPKRSVS 41

RESULT 5
ENTRY    S70399      #type complete
TITLE    zona pellucida glycoprotein C - cat
ORGANISM #formal_name Felis silvestris catus #common_name domestic cat
DATE     28-Oct-1996 #sequence_revision 27-Feb-1997 #text_change
          20-Aug-1999

ACCESSIONS
REFERENCE #authors Harris, J.D.; Hibler, D.W.; Fontenot, G.K.; Hsu, K.T.;
           #journal Yurewicz, E.C.; Sacco, A.G.
           #title DNA Seg. (1994) 4:361-393
           #cross-references EMBL:005778; NID:9458272; PID:AAA74390.1;
           #cross-references MUID:95143578
           #accession S70399
           ##status preliminary
           ##molecule_type mRNA
           ##residues 1-424 ##label HAR
           #cross-references EMBL:005778; NID:9458272; PID:AAA74390.1;
           #cross-references MUID:95143578
           #length 424 #molecular-weight 46853 #checksum 5337

CLASSIFICATION
FEATURE 43-299      #domain ZP domain homology #label ZPH
SUMMARY    #length 424 #molecular-weight 46853 #checksum 5337

```

[illegible]


```

RESULT      15
ENTRY       S52847          #type fragment
TITLE       egg membrane protein ZP3 (clone PCOV638) - common carp
            (fragment)
ORGANISM    #format_name Cyprinus carpio #common_name common carp
DATE        09-Jun-1995 #sequence_revision 21-Jul-1995 #text_change
            20-Aug-1999
ACCESSIONS  S52847
REFERENCE   S52847
            Chang, Y.; Wang, S.; Tsao, C.; Huang, F.
            submitted to the EMBL Data Library, April 1995
            #description Structural analysis and expression of carp ZP3 gene.
            #accession S52847
            ##molecule_type mRNA
            ##residues 1-424 ##label CHA
            ##cross-references EMBL:Z48972; NID:g763077; PIDN:CAB8836.1;
CLASSIFICATION #domain family sperm-binding glycoprotein ZP3; ZP domain
                homology
FEATURE      110-364          #domain ZP domain homology #label ZPH
SUMMARY      #length 424 #checksum 5555
Query Match  24.6%; Score 80; DB 2; Length 424;
Best Local Similarity 27.8%; Pred. No. 4,06e-02;
Matches 10; Conservative 9; Mismatches 16; Indels 1; Gaps 1.
Db 368 GMLADGNHOVSCCD-STCGLDGGAASPSGGYQW 402
OY 1 SWFPVGPFADICCCCKNGDCCTFSHRQRPHVMQW 36
:::|:::||::||::|

```

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 WISE (TM)

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Merch_pp protein - protein database search, using Smith-Waterman algorithm
 Run on: Fri Apr 28 14:23:32 2000; Maspar time 3.68 Seconds
 Tabular output not generated. 332.330 Million cell updates/sec

Title: >US-09-252-828-1
 Description: (1-41) From US09252828.pep
 Perfect Score: 325
 Sequence: 1 SWFPGVQPADICQCCNKNGDCGTPSHSRQPHVNSQMSRSYS 41

Scoring table: PAM 150
 Gap 11

Searched: 82229 seqs, 29864866 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database: swiss-prot38
 1:swissprot

Statistics: Mean 32.196; Variance 46.313; scale 0.695

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	314	96.6	424	1	ZP3A_HUMAN ZONA PELLUCIDA SPERM-B	18,986-61
2	303	93.2	372	1	ZP3B_HUMAN ZONA PELLUCIDA SPERM-B	18,986-58
3	301	92.6	424	1	ZP3A_MACRA ZONA PELLUCIDA SPERM-B	3,076-57
4	253	77.8	424	1	ZP3A_CALSO ZONA PELLUCIDA SPERM-B	2,376-44
5	213	65.5	426	1	ZP3_CANFA ZONA PELLUCIDA SPERM-B	7,336-34
6	197	60.6	422	1	ZP3_MESAU ZONA PELLUCIDA SPERM-B	9,476-30
7	195	60.0	424	1	ZP3_FELCA ZONA PELLUCIDA SPERM-B	3,066-29
8	172	52.9	424	1	ZP3_MOUSE ZONA PELLUCIDA SPERM-B	1,896-23
9	161	49.5	421	1	ZP3_PIG ZONA PELLUCIDA SPERM-B	9,756-21
10	156	48.0	421	1	ZP3_BOVIN ZONA PELLUCIDA SPERM-B	1,626-19
11	131	40.3	415	1	ZP3_RABIT ZONA PELLUCIDA SPERM-B	1,436-13
12	76	23.4	71	1	NXL1_NAJNA LONG NEUROTOXIN 1 (TOX	6,416-02
13	75	23.4	71	1	NXL2_NAJNA LONG NEUROTOXIN 2 (TOX	6,416-02
14	75	23.1	71	1	NXL3_NAJNA LONG NEUROTOXIN 3 (TOX	9,766-02
15	75	23.1	71	1	NXL4_NAJNA LONG NEUROTOXIN 4 (TOX	9,766-02
16	75	23.1	71	1	NXL5_NAJNA LONG NEUROTOXIN 5 (TOX	9,766-02
17	74	22.8	74	1	NXL6_NAJNA LONG NEUROTOXIN 6 (TOX	1,486-01
18	74	22.8	499	1	LIPH_HUMAN ACANTHOPHIN D (POSTSYN	1,486-01
19	73	22.5	999	1	DSG3_HUMAN TRIACYLGLYCEROL LIPASE	2,246-01
20	72	22.2	65	1	DEMOGLEIN 3 PRECURSOR	3,376-01
21	72	22.2	71	1	WEAK NEUROTOXIN 6	3,376-01
22	71	21.8	583	1	NXL1_NAJNA LONG NEUROTOXIN 1 (NEU	5,056-01
23	70	21.5	202	1	HYPOHETICAL 65.0 KD P	7,556-01
					P21_PROTEIN.	

ID	1	STANDARD	PRT	424 AA.
AC	P21754			
DT	01-MAY-1991 (Rel. 18, Created)			
DT	01-MAY-1991 (Rel. 18, Last sequence update)			
DT	15-DEC-1999 (Rel. 39, Last annotation update)			
DE	ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA			
DE	GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3).			
GN	ZP3A OR ZP3.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;			
OC	Eutheria; Primates; Catarrhini; Homidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 90349545.			
RA	CHAMBERLIN M.E., DEAN J.;			
RT	"Human homolog of the mouse sperm receptor."			
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6014-6018(1990).			
RN	[2]			
RP	SEQUENCE OF 329-424 FROM N.A.			
RC	TISSUE-OVARY:			
FX	MEDLINE: 93122771.			
RA	VAN DUIN M., POLMAN J.E., VERKOELEN C.C., BUNSCHOTEN H.,			
RT	MEYERINK J.H., OLIVE W., AITKEN R.J.;			
RT	"Cloning and characterization of the human sperm receptor ligand ZP3:			
RT	evidence for a second polymorphic allele with a different frequency			
RT	in the Caucasian and Japanese populations."			
RL	Genomics 14:1064-1070(1992).			
CC	-1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR			
CC	SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE			
CC	SPECIFICITY OF THE INSEMINATION.			
CC	-1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN			
CC	WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR			
CC	MATRIX.			
CC	-1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.			
CC	-1- SIMILARITY: CONTAINS 1 ZP DOMAIN.			
CC	-1- This SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -			
CC	the European Bioinformatics Institute. There are no restrictions on its			
CC	use by non-profit institutions as long as its content is in no way			
CC	modified and this statement is not removed. Usage by and for commercial			
CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/			
CC	or send an email to license@isb-sib.ch).			
CC	EMBL; M60504; AAA6136.1; -			

DR PIR: A36000; A36000.
 DR MIM: 182889; .
 DR PROSITE: PS00682; ZP_DOMAIN: 1.
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
 KM Extracellular matrix; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 424
 FT DOMAIN 23 387
 FT TRANSMEM 388 408
 FT DOMAIN 409 424
 FT CARBOHYD 45 307
 FT CARBOHYD 125 125
 FT CARBOHYD 147 147
 FT CARBOHYD 226 226
 FT CARBOHYD 272 272
 SO SEQUENCE 424 AA; 47028 MW; 10A13B46 CRC32;

Query Match
 Best Local Similarity 96.6%; Score 314; DB 1; Length 424;
 Matches 39; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 308 SWPVEGPADICCCCKGDCGTPSHSRQPHVMSQMSRSAS 348
 1 SWPVGQPADICCCCKGDCGTPSHSRQPHVMSQMSRSYS 41

RESULT 2
 ID ZP3B_HUMAN STANDARD; PRT; 372 AA.
 AC Q06633;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3B PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3B) (SPERM RECEPTOR) (ZP3).
 GN ZP3B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE; 93122771.
 RA VAN DIN M., POLMAN J.E., VERKOLEN C.C., BUNSCHOTEN H., MEERINK J.H., OLIVE W., AITKEN R.J.;
 RT "Cloning and characterization of the human sperm receptor ligand ZP3: evidence for a second polymorphic allele with a different frequency in the Caucasian and Japanese populations.";
 RL Genomics 14:1064-1070(1992).
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR SPECIES-SPECIFICITY OF THE INSEMINATION, AND MAY CONTRIBUTE TO THE SPERM-ADHESION TO THE ZONA PELLUCIDA.
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR MATRIX.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.
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 CC EMBL; X56777; CAA0095.1; .
 CC EMBL; A18567; CAA01398.1; .
 CC MIM: 195002; .
 DR PROSITE: PS00682; ZP_DOMAIN: 1.
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Glycoprotein; Signal; Sulfatation; Sperm; Receptor;
 KM Extracellular matrix; Multigene family.

FT SIGNAL 1 22
 FT CHAIN 23 372
 FT DOMAIN 45 307
 FT CARBOHYD 125 125
 FT CARBOHYD 147 147
 FT CARBOHYD 226 226
 FT CARBOHYD 272 272
 SO SEQUENCE 372 AA; 41424 MW; 9D714735 CRC32;

Query Match
 Best Local Similarity 93.2%; Score 303; DB 1; Length 372;
 Matches 38; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Db 308 SWPVEGPADICCCCKGDCGTPSHSRQPHVMSQMSRSAS 348
 1 SWPVGQPADICCCCKGDCGTPSHSRQPHVMSQMSRSYS 41

RESULT 3
 ID ZP3A_MACACA STANDARD; PRT; 424 AA.
 AC P53785;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3).
 GN ZP3A OR ZP3.
 OS Macaca radiata (bonnet monkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea; Cercopithecoinae; Macaca.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Ovary;
 RX MEDLINE; 96249321.
 RA KOLHURI S.K., KATL R., BANERJEE K., GUPTA S.K.;
 RT "Nucleotide sequence of cDNA encoding bonnet monkey (Macaca radiata) zona pellucida glycoprotein-zp3.";
 RL Reprod. Fertil. Dev. 7:1209-1212(1995).
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR SPECIES-SPECIFICITY OF THE INSEMINATION, AND MAY CONTRIBUTE TO THE SPERM-ADHESION TO THE ZONA PELLUCIDA.
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR MATRIX.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.
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 CC EMBL; X82639; CAA57961.1; .
 DR PROSITE: PS00682; ZP_DOMAIN: 1.
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
 KM Extracellular matrix; Multigene family.
 FT SIGNAL 1 22
 FT CHAIN 23 424
 FT DOMAIN 23 387
 FT TRANSMEM 388 408
 FT DOMAIN 409 424
 FT CARBOHYD 45 307
 FT CARBOHYD 125 125
 FT CARBOHYD 147 147
 FT CARBOHYD 272 272
 SO SEQUENCE 424 AA; 47040 MW; FSD43A2C CRC32;

Query Match 92.6%; Score 301; DB 1; Length 424;
 Best Local Similarity 90.2%; Pred. No. 3.07e-57;
 Matches 37; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

DB 308 SWPVEGADICCCCKGDCGTPSHSRQPHVMSRSVS 348
 1 SWPVEGADICCCCKGDCGTPSHSRQPHVMSRSVS 41

RESULT 4
 ID ZP3A_CALSO STANDARD; PRT; 424 AA.
 AC P53786;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3A) (ZONA PELLUCIDA PROTEIN C) (SPERM RECEPTOR) (ZP3).
 GN ZP3A OR ZP3.
 OS Callithrix sp. (Marmoset).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrich.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE; 94363314.
 RA THILLAI-KOOTHAN P., VAN DUIN M., AITKEN R.J.;
 RT "Cloning, sequencing and oocyte-specific expression of the marmoset sperm receptor protein, ZP3.";
 RL Zygote 1:93-101(1993).
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE SPECIES-SPECIFICITY OF THE INSEMINATION.
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR MATRIX.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.
 CC -----
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 CC -----
 DR EMBL: S71825; AAB31866.1; -;
 DR PROSITE: PS00682; ZP_DOMAIN; 1.
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Glycoprotein; signal; Sulfatation; Sperm; Receptor; Transmembrane; Extracellular matrix; Multigene family.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 424 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3A.
 FT DOMAIN 23 387 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 388 408 POTENTIAL.
 FT DOMAIN 409 424 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 45 307 ZP.
 FT CARBOHYD 125 125 POTENTIAL.
 FT CARBOHYD 147 147 POTENTIAL.
 FT CARBOHYD 180 180 POTENTIAL.
 FT CARBOHYD 272 272 POTENTIAL.
 FT SEQUENCE 424 AA; 46809 MW; 2FAE3AAD CRC32;

Query Match 77.8%; Score 253; DB 1; Length 424;
 Best Local Similarity 88.2%; Pred. No. 2.37e-44;
 Matches 30; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

DB 308 SWPVEGADICCCCKGDCGTPSHSRQPHVMS 341
 1 SWPVEGADICCCCKGDCGTPSHSRQPHVMS 34

Query Match 65.5%; Score 213; DB 1; Length 426;
 Best Local Similarity 60.0%; Pred. No. 7.33e-34;
 Matches 24; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

DB 307 WYVEGADICCCCKGDCGTPSHSRQPHVMSRSVS 346
 2 WYVEGADICCCCKGDCGTPSHSRQPHVMSRSVS 41

RESULT 5
 ID ZP3_CANFA STANDARD; PRT; 426 AA.
 AC P48831;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-DEC-1999 (Rel. 39, Last annotation update)
 DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3 PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3) (SPERM RECEPTOR) (ZONA PELLUCIDA PROTEIN C).
 GN ZP3 OR ZPC.
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX MEDLINE; 95143578.
 RA HARRIS J.D., HIBLER D.W., FONTENOT G.K., HSU K.T., YUREWICZ E.C.,
 RA SACC0 A.G.;
 RT "Cloning and characterization of zona pellucida genes and cDNAs from a variety of mammalian species: the ZPA, ZPB and ZPC gene families.";
 RL DNA Seq. 4:361-393(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARY;
 RX OKAZAKI Y., SUGIMOTO M.;
 RA Submitted (JAN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE SPECIES-SPECIFICITY OF THE INSEMINATION (BY SIMILARITY).
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR MATRIX.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.
 CC -----
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 CC -----
 DR EMBL: U05780; AAA74387.1; -;
 DR PROSITE: PS00682; ZP_DOMAIN; 1.
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Glycoprotein; signal; Sulfatation; Sperm; Receptor; Transmembrane; Extracellular matrix; Multigene family.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 426 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.
 FT DOMAIN 23 385 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 386 406 POTENTIAL.
 FT DOMAIN 407 426 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 43 305 ZP.
 FT CARBOHYD 123 123 POTENTIAL.
 FT CARBOHYD 145 145 POTENTIAL.
 FT CARBOHYD 244 244 POTENTIAL.
 FT CARBOHYD 227 227 L -> P (IN REF. 2).
 FT CONFLICT 307 307 W -> S (IN REF. 2).
 FT CONFLICT 343 343 K -> R (IN REF. 2).
 FT SEQUENCE 426 AA; 47367 MW; 9CB10DE2 CRC32;

RESULT	6		STANDARD:	PRT:	422 AA.
ID	ZP3_MESAU				
AC	P23491:				
DT	01-NOV-1991 (Rel. 20, Created)				
DT	01-FEB-1996 (Rel. 33, Last sequence update)				
DT	15-DEC-1999 (Rel. 39, Last annotation update)				
DE	ZONA PELLUCIDA SPERM-BINDING PROTEIN 3 PRECURSOR (ZONA PELLUCIDA GLYCOPROTEIN ZP3) (SPERM RECEPTOR) (ZONA PELLUCIDA PROTEIN C).				
GN	ZP3.				
OS	Mesocricetus auratus (golden hamster).				
OC	Eumetazoa; Chordata; Craniata; Vertebrate; Mammalia;				
CC	Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae; Mesocricetus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-Ovary:				
RX	MEDLINE: 91078540.				
RA	KINDOCH R.A., RUTZ-SELLER B., WASSARMAN P.M.;				
RT	"Genomic organization and polypeptide primary structure of zona pellucida glycoprotein hzp3, the hamster sperm receptor.";				
RL	Dev. Biol. 142:414-421(1991).				
CC	-I- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR SPECIFIC ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE SPECIES-SPECIFICITY OF THE INSEMINATION.				
CC	-I- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.				
CC	-I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR MATRIX.				
CC	-I- TISSUE SPECIFICITY: OOCYTES.				
CC	-I- DEVELOPMENTAL STAGE: GROWING OOCYTES.				
CC	-I- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES.				
CC	-I- SIMILARITY: CONTAINS 1 ZP DOMAIN.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@sib-sib.ch). -----				
DR	EMBL: M63629; AAA37079.1; -				
DR	PROSITE; PS00682; ZP_DOMAIN; 1.				
DR	PFAM; PF00100; zona_pellucida; 1.				
KW	Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane; Extracellular matrix.				
FT	SIGNAL	1	22	POTENTIAL.	
FT	CHAIN	23	422	ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.	
FT	DOMAIN	23	386	EXTRACELLULAR (POTENTIAL).	
FT	TRANSMEM	387	407	POTENTIAL.	
FT	DOMAIN	408	422	CYTOLASMIC (POTENTIAL).	
FT	DOMAIN	45	306	ZP.	
FT	DOMAIN	119	158	PRO-RICH.	
FT	DOMAIN	208	257	PRO-RICH.	
FT	CARBOHYD	146	146	POTENTIAL.	
FT	CARBOHYD	271	271	POTENTIAL.	
FT	CARBOHYD	302	302	POTENTIAL.	
SO	SEQUENCE	422 AA;	45827 MM;	22B720FS CRC32;	

Query Match 60.6%; Score 197; DB 1; Length 422;
Best Local Similarity 56.1%; Pred. No. 9,47e-30;
Matches 23; Conservative 11; Mismatches 7; Indels 0; Gaps 0;

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Db      307   SMSPEGDAEVCGSSSGCGSSSRFYQAHGVSONPKMSAS 347
        |||::|||::|||::|||||::|||::|||::|||::|||
Oy      1     SMFPVGADPDICCNKGDCGTGSRSRKPVMWSOMSSVS 41
    
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RESULT 7
ID ZP3_FELCA STANDARD: PRT: 424 AA.
AC P48832:
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)

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DE 15-DEC-1999 (Rel. 39, Last annotation update)
DT ZONA PELLUCIDA SPERM-BINDING PROTEIN 3 PRECURSOR (ZONA PELLUCIDA
DE GLYCOPROTEIN ZP3) (SPERM RECEPTOR) (ZONA PELLUCIDA PROTEIN C).
CN ZP3 OR ZPC.
OS Felis silvestris catus (Cat).
RA Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
RX Eutheria; Carnivora; Fissipedia; Felidae; Felis.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA MEDLINE: 95143578.
RA HARRIS J.D., HIBLER D.W., FONTENOT G.K., HSU K.T., YUREWICZ E.C.,
RA SACC0 A.G. ;
RT Cloning and characterization of zona pellucida genes and cDNAs from
RT a variety of mammalian species: the ZPA, ZPB and ZPC gene families." ;
RL DNA Seq. 4:361-393(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-OVARY;
RA OKAZAKI Y., SUGIMOTO M. ;
RL Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR
CC SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE
CC SPECIFIC-SPECIFICITY OF THE INSEMINATION (BY SIMILARITY).
CC -I- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN
CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR
CC MATRIX.
CC -I- PFM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES (BY
CC SIMILARITY).
CC -I- SIMILARITY: CONTAINS 1 ZP DOMAIN.
CC -----
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CC -----
CC DR EMBL; U05778; AAA74390.1; -
CC DR EMBL; D45068; BAA08096.1; -
CC DR PROSITE; PS00682; ZP_DOMAIN; FALSE_NEG.
CC DR PFM; PFM0100; zona_pellucida; 1.
CC KM Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
CC KM Extracellular matrix; Multigene family.
CC FT SIGNAL 1 22
CC FT CHAIN 23 424
CC FT DOMAIN 23 383
CC FT TRANSMEM 384 404
CC FT DOMAIN 405 424
CC FT DOMAIN 43 305
CC FT CARBOHYD 52 52
CC FT CARBOHYD 123 123
CC FT CARBOHYD 145 145
CC FT CONFLICT 72 72
CC FT CONFLICT 264 264
CC FT SEQUENCE 424 AA; 46853 MM; B356f362 CRC32;
CC SO
DB 307 WPPVGGPADIQCCKKSGGLGGRSMRSHDTRWKKKAS 346
DY 2 WPPVGGPADIQCCKKSGGLGGRSHSRKPPHVMQSMRSRVS 41
Query Match 60.0%; Score 195; DB 1; Length 424;
Best Local Similarity 55.0%; Pred. No. 3,06e-29;
Matches 22; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

RESULT 8 STANDARD: PRT; 424 AA.
AC 01-JUL-1989 (Rel. 11, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)

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FT DOMAIN 22 381 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 382 402 POTENTIAL.
FT DOMAIN 403 421 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 44 306 ZP.
FT CARBOHYD 124 146 POTENTIAL.
FT CARBOHYD 146 146 POTENTIAL.
FT CARBOHYD 179 179 POTENTIAL.
FT CARBOHYD 271 271 POTENTIAL.
FT CARBOHYD 271 271 MISSING (IN REF. 2).
FT CONFLICT 101 101 D -> V (IN REF. 2).
FT CONFLICT 107 107 V -> G (IN REF. 2).
FT CONFLICT 163 164 P -> A (IN REF. 2).
FT CONFLICT 404 404
SO SEQUENCE 421 AA; 46239 MW; B8702084 CRC32;

Query Match
Best Local Similarity 49.5%; Score 161; DB 1; Length 421;
Matches 19; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

Db 308 WSPVGPADICCCCKGDCGTPSHSR 334
Qy 2 WEPVGPADICCCCKGDCGTPSHSR 28

RESULT 10
ID ZP3 BOVIN STANDARD: PRT; 421 AA.
AC P48830;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-DEC-1999 (Rel. 39, Last annotation update)
DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3 PRECURSOR (ZONA PELLUCIDA
DE GLYCOPROTEIN ZP3) (SPERM RECEPTOR) (ZONA PELLUCIDA PROTEIN C).
GN ZP3 OR ZPC.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia;
OC Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae;
OC Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE: 95143578.
RA HARRIS J.D., HIBLER D.W., FONTENOT G.K., HSU K.T., YUREWICZ E.C.,
RA SACC0 A.G.;
"Cloning and characterization of zona pellucida genes and cDNAs from
a variety of mammalian species: the ZPA, ZPB and ZPC gene families.";
RT DNA Seq. 4:361-393(1994).
RL
CC -1- FUNCTION: FUNCTIONS AS A SPERM-RECEPTOR. IT IS RESPONSIBLE FOR
CC SPERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE
CC SPECIES-SPECIFICITY OF THE INSEMINATION (BY SIMILARITY).
CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN
CC WHICH ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR
CC MATRIX.
CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES (BY
CC SIMILARITY).
CC -1- SIMILARITY: CONTAINS 1 ZP DOMAIN.
CC
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CC
CC EMBL: U05775; AAA74385.1; -.
CC DR PROSITE: PS00682; ZP_DOMAIN: 1.
CC DR PFAM: PF00100; zona_pellucida: 1.
CC KW Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
CC Extracellular matrix; Multigene family.
CC FT SIGNAL 1 22
CC FT CHAIN 23 421 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.
CC FT DOMAIN 23 381 EXTRACELLULAR (POTENTIAL).
CC FT TRANSMEM 382 402 POTENTIAL.

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FT DOMAIN 403 421 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 44 306 ZP.
FT CARBOHYD 124 146 POTENTIAL.
FT CARBOHYD 146 146 POTENTIAL.
FT CARBOHYD 179 179 POTENTIAL.
FT CARBOHYD 271 271 POTENTIAL.
SO SEQUENCE 421 AA; 46545 MW; B52724BA CRC32;

Query Match
Best Local Similarity 48.0%; Score 156; DB 1; Length 421;
Matches 17; Conservative 8; Mismatches 5; Indels 0; Gaps 0;

Db 308 WSPVGPADICCCCKGDCGTPSHSR 337
Qy 2 WEPVGPADICCCCKGDCGTPSHSR 31

RESULT 11
ID ZP3 RABIT STANDARD: PRT; 415 AA.
AC P48833;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE ZONA PELLUCIDA SPERM-BINDING PROTEIN 3 PRECURSOR (ZONA PELLUCIDA
DE GLYCOPROTEIN ZP3) (SPERM RECEPTOR) (ZONA PELLUCIDA PROTEIN C)
DE (FRAGMENT).
GN ZP3 OR ZPC.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary;
RX MEDLINE: 95143578.
RA HARRIS J.D., HIBLER D.W., FONTENOT G.K., HSU K.T., YUREWICZ E.C.,
RA SACC0 A.G.;
"Cloning and characterization of zona pellucida genes and cDNAs from
a variety of mammalian species: the ZPA, ZPB and ZPC gene families.";
RT DNA Seq. 4:361-393(1994).
RL
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL: U05782; AAA74392.1; -.
CC DR PROSITE: PS00682; ZP_DOMAIN: 1.
CC DR PFAM: PF00100; zona_pellucida: 1.
CC KW Glycoprotein; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
CC Extracellular matrix; Multigene family.
CC FT SIGNAL 1 18
CC FT CHAIN 19 415 ZONA PELLUCIDA SPERM-BINDING PROTEIN 3.
CC FT TRANSMEM 379 399 EXTRACELLULAR (POTENTIAL).
CC FT DOMAIN 400 415 CYTOPLASMIC (POTENTIAL).
CC FT DOMAIN 41 301 ZP.
CC SO SEQUENCE 415 AA; 44987 MW; BA52674 CRC32;

Query Match
Best Local Similarity 40.3%; Score 131; DB 1; Length 415;
Matches 16; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

Db 302 SWAPVGSADICCCCKGDCGTPSHSR 333
Qy 1 WEPVGPADICCCCKGDCGTPSHSR 31

RESULT 12
ID NX1L_MAJNA STANDARD: PRT; 71 AA.

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P25668: P01392;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE LONG NEUROTOXIN 1 (TOXIN A).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
 OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
 OC Naja.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM:
 EX MEDLINE: 7205125.
 EA NAKAI K., SASAKI T., HAYASHI K.;
 RT "Amino acid sequence of toxin A from the venom of the Indian cobra
 (Naja naja)."
 CC Biochem. Biophys. Res. Commun. 44:893-897(1971).
 CC -I- MISCELLANEOUS: LD(50) IS 0.15 MG/KG BY SUBCUTANEOUS INJECTION.
 DR PIR: A01663; NZNJ11.
 DR HSSP: P01391; ICTX.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 DR PFAM: PF00087; toxin; 1.
 KW Venom; Neurotoxin; Multigene family.
 FT DISULFID 3 20
 FT DISULFID 14 41
 FT DISULFID 26 30
 FT DISULFID 45 56
 FT DISULFID 57 62
 SQ SEQUENCE 71 AA; 7847 MW; 27FE079A CRC32;
 Query Match 23.48; Score 76; DB 1; Length 71;
 Best Local Similarity 42.38; Pred. No. 6.41e-02;
 Matches 11; Conservative 5; Mismatches 8; Indels 2; Gaps 2;
 DB 48 VRTGVDI-OCCSTDCCD-PEPTRRRP 71
 QY 5 VQGPADICCCCKNGDCGTPSHSRQP 30
 RESULT 13
 ID NX12_NAJNA STANDARD; PRT; 71 AA.
 AC P25669: P01392;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LONG NEUROTOXIN 2 (TOXIN B).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
 OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
 OC Naja.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM:
 EX MEDLINE: 77048940.
 EA OHTA M., SASAKI T., HAYASHI K.;
 RT "The primary structure of toxin B from the venom of the Indian cobra
 Naja naja."
 CC FEBS Lett. 72:161-166(1976).
 CC PIR: A01663; NZNJ11.
 DR HSSP: P01391; ICTX.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 DR PFAM: PF00087; toxin; 1.
 KW Venom; Neurotoxin; Multigene family.
 FT DISULFID 3 20
 FT DISULFID 14 41
 FT DISULFID 26 30
 FT DISULFID 45 56
 FT DISULFID 57 62
 SQ SEQUENCE 71 AA; 7821 MW; 2C93A754 CRC32;
 Query Match 23.48; Score 76; DB 1; Length 71;
 Best Local Similarity 42.38; Pred. No. 6.41e-02;
 Matches 11; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

DB 48 VRTGVDI-OCCSTDCCD-PEPTRRRP 71
 QY 5 VQGPADICCCCKNGDCGTPSHSRQP 30
 RESULT 14
 ID NX13_NAJNA STANDARD; PRT; 71 AA.
 AC P25671;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE LONG NEUROTOXIN 3 (TOXIN C).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
 OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
 OC Naja.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM:
 EA OHTA M., SASAKI T., HAYASHI K.;
 RT "The primary structure of toxin C from the venom of the Indian cobra
 (Naja naja)."
 CC Chem. Pharm. Bull. 29:1458-1475(1981).
 CC -I- MISCELLANEOUS: LD(50) IS 0.10 TO 0.15 MG/KG BY SUBCUTANEOUS
 INJECTION.
 DR HSSP: P01391; ICTX.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 DR PFAM: PF00087; toxin; 1.
 KW Venom; Neurotoxin; Multigene family.
 FT DISULFID 3 20
 FT DISULFID 14 41
 FT DISULFID 26 30
 FT DISULFID 45 56
 FT DISULFID 57 62
 SQ SEQUENCE 71 AA; 7833 MW; 41B7B968 CRC32;
 Query Match 23.18; Score 75; DB 1; Length 71;
 Best Local Similarity 42.38; Pred. No. 9.76e-02;
 Matches 11; Conservative 4; Mismatches 9; Indels 2; Gaps 2;
 DB 48 VRTGVDI-OCCSTDCCD-PEPTRRRP 71
 QY 5 VQGPADICCCCKNGDCGTPSHSRQP 30
 RESULT 15
 ID NX14_NAJNA STANDARD; PRT; 71 AA.
 AC P25672;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-MAY-1992 (Rel. 22, Last annotation update)
 DE LONG NEUROTOXIN 4 (TOXIN D).
 OS Naja naja (Indian cobra).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;
 OC Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae;
 OC Naja.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-VENOM:
 EX MEDLINE: 82113654.
 EA OHTA M., SASAKI T., HAYASHI K.;
 RT "The amino acid sequence of toxin D isolated from the venom of Indian
 cobra (Naja naja)."
 CC Biochim. Biophys. Acta 671:123-128(1981).
 CC -I- MISCELLANEOUS: LD(50) IS 0.22 MG/KG BY SUBCUTANEOUS INJECTION.
 DR HSSP: P01391; ICTX.
 DR PROSITE: PS00272; SNAKE_TOXIN; 1.
 DR PFAM: PF00087; toxin; 1.
 KW Venom; Neurotoxin; Multigene family.
 FT DISULFID 3 20
 FT DISULFID 14 41
 FT DISULFID 26 30
 FT DISULFID 45 56
 FT DISULFID 57 62
 SQ SEQUENCE 71 AA; 7821 MW; 2C93A754 CRC32;
 Query Match 23.48; Score 76; DB 1; Length 71;
 Best Local Similarity 42.38; Pred. No. 6.41e-02;
 Matches 11; Conservative 5; Mismatches 8; Indels 2; Gaps 2;

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Title: >US-09-252-828-1
 Description: (1-41) from US09252828.pep
 Perfect Score: 325
 Sequence: 1 SMFPVQGPADICCCCKNGDCTPSHRSRPHVMSQMSRSVS 41

Scoring table: PAM 150
 Gap 11

Searched: 225878 seqs, 69334122 residues

Post-processing: Minimum Match 0%
 Listing first 45 summaries

Database:

sptrembl12
 1:sp_archaea 2:sp_bacteria 3:sp_fungi 4:sp_human
 5:sp_invertebrate 6:sp_mammal 7:sp_mhc 8:sp_organelle
 9:sp_phase 10:sp_plant 11:sp_rodent 12:sp_unclassified
 13:sp_vertebrate 14:sp_virus

Statistics: Mean 31.925; Variance 46.387; scale 0.688

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	287	88.3	210	4	POM-ZP3	1.23e-52
2	167	51.4	424	11	ZONA PELUCIDA SPERM-B	1.16e-21
3	151	46.5	434	13	ZONA PELUCIDA C GLYCO	8.72e-18
4	151	46.5	460	13	GP43	8.72e-18
5	132	40.6	422	6	ZONA PELUCIDA 3 PROTE	2.57e-13
6	124	38.2	446	13	OUAIL ZPC	1.74e-11
7	123	37.8	444	13	ZPC	2.93e-11
8	86	26.5	934	2	LIPA TRANSCRIPTIONAL A	2.13e-03
9	82	25.2	428	13	ZP3	1.26e-02
10	81	24.9	422	13	FOR ZP3 (CLONE PCOV328	1.96e-02
11	80	24.6	414	13	ZONA PELUCIDA PROTEIN	3.03e-02
12	80	24.6	419	13	ZP3 GENE	3.03e-02
13	80	24.6	424	13	ZP3 (CLONE PCOV638) (F	2.54e-01
14	75	23.1	295	5	T02B11.1 PROTEIN	2.54e-01
15	75	23.1	843	2	NUOG, NADH DEHYDROGENA	3.84e-01
16	74	22.8	499	4	HEPATIC TRIGLYCERIDE L	3.84e-01
17	74	22.8	544	1	DNA ORF1-ORF5	3.84e-01
18	73	22.5	586	5	TISSUE POLARITY PROTEI	5.80e-01
19	72	22.2	338	4	CASPASE-ACTIVATED NUCL	8.72e-01
20	72	22.2	338	4	DNA FRAGMENTATION FACT	8.72e-01

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
21	72	22.2	344	11	DNAse INHIBITED BY DNA	8.72e-01
22	72	22.2	745	2	ISOCITRATE DEHYDROGENA	8.72e-01
23	71	21.8	368	4	TRANSFORMATION-RELATED	1.31e+00
24	71	21.8	490	2	GLUTAMATE SYNTHASE SMA	1.31e+00
25	71	21.8	592	13	7-TRANSMEMBRANE PROTEI	1.31e+00
26	71	21.8	1394	5	SIMILARITY TO AN AMP-B	1.31e+00
27	70	21.5	91	2	FERREDOXIN	1.95e+00
28	70	21.5	218	2	HYPOHETICAL 23.3 KD P	1.95e+00
29	70	21.5	304	4	CAGH44 (FRAGMENT)	1.95e+00
30	70	21.5	317	2	HYPOHETICAL 34.6 KD P	1.95e+00
31	70	21.5	498	13	ESR4	1.95e+00
32	70	21.5	626	11	FRIZZLED-1	1.95e+00
33	70	21.5	641	11	FRIZZLED-1	1.95e+00
34	70	21.5	647	4	FRIZZLED-1	1.95e+00
35	70	21.5	749	5	CODED FOR BY C. ELEGAN	1.95e+00
36	70	21.5	2090	5	CODED FOR BY C. ELEGAN	1.95e+00
37	70	21.5	2153	5	CODED FOR BY C. ELEGAN	1.95e+00
38	69	21.2	108	2	HYPOHETICAL 11.8 KD P	2.90e+00
39	69	21.2	118	14	TWO FIBERS, PROTEIN PV	2.90e+00
40	69	21.2	127	10	OSMOTIN (FRAGMENT)	2.90e+00
41	69	21.2	127	10	C TERMINUS OF HSV US3	2.90e+00
42	69	21.2	147	14	GAG-LIKE POLYPROTEIN (2.90e+00
43	69	21.2	167	3	JUS1	2.90e+00
44	69	21.2	1124	13	DSRNA ADENOSINE DEAMIN	2.90e+00
45	69	21.2	1339	5	BETA-1,3-D-GLUCAN BIND	2.90e+00

ALIGNMENTS

Result No.	Score	Query Match	Length	ID	Description	Pred. No.
1	287	88.3%	210	4	POM-ZP3	1.23e-52
2	167	51.4%	424	11	ZONA PELUCIDA SPERM-B	1.16e-21
3	151	46.5%	434	13	ZONA PELUCIDA C GLYCO	8.72e-18
4	151	46.5%	460	13	GP43	8.72e-18
5	132	40.6%	422	6	ZONA PELUCIDA 3 PROTE	2.57e-13
6	124	38.2%	446	13	OUAIL ZPC	1.74e-11
7	123	37.8%	444	13	ZPC	2.93e-11
8	86	26.5%	934	2	LIPA TRANSCRIPTIONAL A	2.13e-03
9	82	25.2%	428	13	ZP3	1.26e-02
10	81	24.9%	422	13	FOR ZP3 (CLONE PCOV328	1.96e-02
11	80	24.6%	414	13	ZONA PELUCIDA PROTEIN	3.03e-02
12	80	24.6%	419	13	ZP3 GENE	3.03e-02
13	80	24.6%	424	13	ZP3 (CLONE PCOV638) (F	2.54e-01
14	75	23.1%	295	5	T02B11.1 PROTEIN	2.54e-01
15	75	23.1%	843	2	NUOG, NADH DEHYDROGENA	3.84e-01
16	74	22.8%	499	4	HEPATIC TRIGLYCERIDE L	3.84e-01
17	74	22.8%	544	1	DNA ORF1-ORF5	3.84e-01
18	73	22.5%	586	5	TISSUE POLARITY PROTEI	5.80e-01
19	72	22.2%	338	4	CASPASE-ACTIVATED NUCL	8.72e-01
20	72	22.2%	338	4	DNA FRAGMENTATION FACT	8.72e-01

RP SEQUENCE FROM N.A.
 RC STRAIN-WISTAR; TISSUE-OVARY;
 RA MACDUFF P.E., KERR L.E., AITKEN R.J.;
 RL J. Reprod. Fertil. Abstr. Ser. 18:86-86(1996).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-OVARY;
 RA AKATSUKA K., YOSHIDA-KOMIYA H., TULSIANT D.P., ORGEBIN-CRIST M.,
 HIROI M., ARAKI Y.;
 RL Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: FUNCTIONS AS A SPEERM-RECEPTOR. IT IS RESPONSIBLE FOR
 CC SPEERM-ADHESION TO THE ZONA PELLUCIDA, AND MAY CONTRIBUTE TO THE
 CC SPECIES-SPECIFICITY OF THE INSEMINATION.
 CC -1- SUBUNIT: ZP3 FORMS WITH ZP1 AND ZP2 THE ZONA PELLUCIDA, IN WHICH
 CC ZP2 AND ZP3 COMPLEX INTO COPOLYMERS CROSS-LINKED BY ZP1.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. EXTRACELLULAR
 CC MATRIX.
 CC -1- PTM: SULFATED GLYCOPROTEIN WITH O-LINKED OLIGOSACCHARIDES (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: CONTAINS A ZP DOMAIN, WHICH CURRENTLY HAS BEEN FOUND
 CC IN ZP2, ZP3, GP2, TGF-3 AND UROMODULIN.
 CC EMBL: Y10823; CAU1787.1; -;
 CC EMBL: D78482; BAA24456.1; -;
 CC DR PROSITE: PS00682; ZP_DOMAIN; FALSE_NEG.
 CC DR PFAM: PF00100; zona_pellucida; 1.
 CC DR PRINTS: PR00023; ZPELLUCIDA.
 CC DR GLYCOPROTEIN; Signal; Sulfatation; Sperm; Receptor; Transmembrane;
 CC KW Extracellular matrix.
 FT SIGNAL 1
 FT CHAIN 16
 FT DOMAIN 17 424
 FT DOMAIN 17 387
 FT TRAMEM 388 408
 FT DOMAIN 409 424
 FT DOMAIN 45
 FT DOMAIN 329 308
 FT DOMAIN 329 334
 FT CARBOHYD 146
 FT CARBOHYD 273 273
 FT CARBOHYD 304 304
 FT CARBOHYD 327 327
 FT CARBOHYD 330 330
 FT CONFLICT 55
 FT CONFLICT 112
 FT CONFLICT 412
 FT CONFLICT 412
 FT SEQUENCE 424 AA; 45901 MW; E8EC90D7 CRC32;
 Query Match 51.4%; Score 167; DB 11; Length 424;
 Best Local Similarity 51.2%; Pred. No. 1,16e-21;
 Matches 21; Conservative 10; Mismatches 10; Indels 0; Gaps 0;
 Db 309 SWLPVEGDADICCCGNGCNSSEFEETHEPAQWSTLVS 349
 OY 1 SWFPVQGPADICQCCCKNGDC-GTPSHSRQ-PHYV-SQMSRSVS 41
 RESULT 3
 ID 091675 PRELIMINARY; PRT; 454 AA.
 AC 091675;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-FEB-1997 (TREMblrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE ZONA PELLUCIDA C GLYCOPROTEIN PRECURSOR.
 GN XL2PC.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 CC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
 CC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA HEHRICK J.L., YANG J.C.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U44952; AAB39079.1; -;
 DR PFAM: PF00100; zona_pellucida; 1.
 KW Signal.

FT SIGNAL 1 21
 FT CHAIN 22 454
 FT SEQUENCE 454 AA; 49569 MW; 57E58E90 CRC32;
 SO
 Query Match 46.5%; Score 151; DB 13; Length 454;
 Best Local Similarity 46.3%; Pred. No. 8.72e-18;
 Matches 19; Conservative 11; Mismatches 8; Indels 3; Gaps 3;
 Db 330 SMSPLQSPNISCDDTGVCVSPGSRRLGPFSGSRNQ 370
 OY 1 SWFPVQGPADICQCCCKNGDC-GTPSHSRQ-PHYV-SQMSR 38
 RESULT 4
 ID 091728 PRELIMINARY; PRT; 460 AA.
 AC 091728;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-NOV-1998 (TREMblrel. 08, Last annotation update)
 DE GP43.
 OS Xenopus laevis (African clawed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 CC Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae; Xenopodinae;
 CC Xenopus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-OVARIES FROM HCG-TREATED FEMALES;
 RX MEDLINE; 98013448.
 RA KUBO H., KAMANO T., TSUBUKI S., KAMASHIMA S., KATAGIRI C., SUZUKI A.;
 RT "A major glycoprotein of Xenopus egg vitelline envelope, gp41, is a
 RT frog homolog of mammalian ZP3."
 RL Dev. Growth Differ. 39:405-417(1997).
 DR EMBL: D86568; BAA13117.1; -;
 DR PFAM: PF00100; zona_pellucida; 1.
 DR SEQUENCE 460 AA; 50084 MW; ADD6CD59 CRC32;
 Query Match 46.5%; Score 151; DB 13; Length 460;
 Best Local Similarity 46.3%; Pred. No. 8.72e-18;
 Matches 19; Conservative 11; Mismatches 8; Indels 3; Gaps 3;
 Db 336 SMSPLQSPNISCDDTGVCVSPGSRRLGPFSGSRNQ 376
 OY 1 SWFPVQGPADICQCCCKNGDC-GTPSHSRQ-PHYV-SQMSR 38
 RESULT 5
 ID 077685 PRELIMINARY; PRT; 422 AA.
 AC 077685;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-NOV-1999 (TREMblrel. 12, Last annotation update)
 DE ZONA PELLUCIDA 3 PROTEIN.
 GN ZP3.
 OS Trichosurus vulpecula (Brush-tailed possum).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 CC Metatheria; Diprotodontia; Phalangeridae; Trichosurus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MCCARTNEY C.A., MATE K.E.;
 RT "Cloning and characterization of a zona pellucida 3 cDNA from a
 RT marsupial, the brush-tail possum Trichosurus vulpecula."
 RL Zygote 0:0-0(1998).
 DR EMBL: AF079524; AAC28736.1; -;
 DR PFAM: PF00100; zona_pellucida; 1.
 DR PRINTS: PR00023; ZPELLUCIDA.
 DR SEQUENCE 422 AA; 45714 MW; 69216067 CRC32;
 Query Match 40.6%; Score 132; DB 6; Length 422;
 Best Local Similarity 51.7%; Pred. No. 2.57e-13;
 Matches 15; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 Db 314 WLPEGPADICCCGTCGTCISLSSRRK 342
 OY 1 SWFPVQGPADICQCCCKNGDC-GTPSHSRQ-PHYV-SQMSR 38


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QY      2 WFPVVGADICCCCKNGDCGTPSHSRQP 30

RESULT      6
ID          AC       PRELIMINARY;           PRT;     446 AA.
AC      073670;
BT      01-AUG-1998 (TREMBlrel.. 07, Created)
DT      01-AUG-1998 (TREMBlrel.. 07, Last sequence update)
DR      01-NOV-1999 (TREMBlrel.. 12, Last annotation update)
DE      QOALF ZPC.
NC      Coturnix coturnix japonica (Japanese quail).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
ON      Neognathae; Galliformes; Phasianidae; Phasianinae; Coturnix.
[1]
SEQUENCE FROM N.A.
3P      KONO T., TSUDA T., AOKI N., KITAJIMA K., MATSUDA T.;
3L      Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
JR      EMBL: AB012606; BAA25637.1; -
CR      PFAM: PF00100; zona pellucida; 1.
PR      PRINTS: PRO0023; ZPELLUCIDA.
30      SEQUENCE    446 AA;   47621 MW;   599DCBC9 CRC32;

Query Match              38.2%; Score 124; DB 13; Length 446;
Best Local Similarity 42.9%; Pred. No. 1.74e+11;
Matches 12; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

Db      330 TWVPVEGRDVCSCCTGCNCDARALAR 357
        :|::||::|:|::|::|::|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
QY      1 SWFPVGGPADICCCCKNGDCGTPSHSRR 28

RESULT      7
ID          AC       PRELIMINARY;           PRT;     444 AA.
AC      P79762;
BT      01-MAY-1997 (TREMBlrel.. 03, Created)
DT      01-MAY-1997 (TREMBlrel.. 03, Last sequence update)
DR      01-NOV-1999 (TREMBlrel.. 12, Last annotation update)
DE      ZPC.
NC      Gallus gallus (Chicken).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria; Aves;
ON      Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
[1]
SEQUENCE FROM N.A.
RA      TAKUCHI Y., NISHITURA K., ADACHI T., AOKI N., MATUDA T.;
RT      "Isolation and cDNA cloning of chicken zpc.";
RL      Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
DR      EMBL: D89097; BAA13760.1; -.
PR      PFMF: PF00100; zona pellucida; 1.
DR      PRINTS: PRO0023; ZPELLUCIDA.
SO      SEQUENCE    444 AA;   47556 MW;   B40FLBDA CRC32;

Query Match              37.8%; Score 123; DB 13; Length 444;
Best Local Similarity 42.9%; Pred. No. 2.93e+11;
Matches 12; Conservative 7; Mismatches 9; Indels 0; Gaps 0;

Db      330 TWVPVEGRDVCNCGTCGNCEAALRR 357
        :||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
QY      1 SWFPVGGPADICCCCKNGDCGTPSHSRR 28

RESULT      8
ID          AC       PRELIMINARY;           PRT;     934 AA.
AC      005478;
BT      01-JUL-1997 (TREMBlrel.. 04, Created)
DT      01-JUL-1997 (TREMBlrel.. 04, Last sequence update)
DR      01-NOV-1998 (TREMBlrel.. 08, Last annotation update)
DE      LIPA TRANSCRIPTIONAL ACTIVATOR.
GN      LIPR.
OS      Streptomyces sp.
OC      Bacteria; Firmicutes; Actinobacteriae; Actinobacteridae;
ON      Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
RN      [1]
SEQUENCE FROM N.A.
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Query Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
26.5%;	29.7%;	86;	2;	934;	1;	1
Matches 11;	Conservative 13;	Mismatches 12;				
DB 640	SVGGEGCAACAHCAALAGANPHGLAQPATATATARG 676					
Oy 4	PVGGADICOC-CNKGGCGPSSHRSRPPHVMQMSRS 39					
RESULT 9	PRELIMINARY;	PRT;	428 AA.			
ID 091984						
AC 091984;						
DT 01-NOV-1996 (TREMBlrel. 01, Created)						
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)						
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)						
DE zp3.						
GN zp3.						
OS Carassius auratus (Goldfish).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;						
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;						
OC Cyprinidae; Cyprinidae; Cyprinidae; Carassius.						
CC [1]						
RP SEQUENCE FROM N.A.						
RC TISSUE-Ovary;						
RA CHANG Y., WANG S., TSAO C., HUANG F.;						
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.						
DR EMBL; Z49974; CA88838.1; -						
DR EMBL; L41636; AB41819.1; -						
DR PFM; PF00100; zone_pellucida; 1.						
SO SEQUENCE 428 AA; 46651 MW; 59861e52 CRC32;						
Query Match	25.2%;	Score 82;	DB 13;	Length 428;		
Best Local Similarity	30.4%;	Pred. NO. 1.26e-02;				
Matches 7;	Conservative 10;	Mismatches 5;	Indels 1;	Gaps 1		
DB 379	GMLADGNHGVCGCCD-STCASP 400					
OY 1	SMFVGGADICOC-CNKGGCGPSSHRSRPPHVMQMSRS 23					
RESULT 10	PRELIMINARY;	PRT;	422 AA.			
ID 092023						
AC 092023;						
DT 01-NOV-1996 (TREMBlrel. 01, Created)						
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)						
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)						
DE 01-NOV-1998 (TREMBlrel. 08, Last annotation update)						
DE zp3	(Clone PCOV328).					
GN zp3.						
OS Cyprinus carpio (Common carp).						
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;						
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;						
OC Cyprinidae; Cyprinidae; Cyprinidae; Cyprinus.						

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RP SEQUENCE FROM N.A.
RC TISSUE-Ovary:
RA CHANG Y., WANG S., TSAO C., HUANG F.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary:
RA CHANG Y.S., WANG S.C., TSAO C.C., HUANG F.L.;
RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z48973; CA88837.1;
DR EMBL: L41639; AAB41822.1;
DR PFM: PFM0100; zona_pellucida.1.
SQ SEQUENCE 422 AA; 46187 MW; EF15E170 CRC32;

Query Match 24.9%; Score 81; DB 13; Length 422;
Best Local Similarity 30.6%; Pred. NO. 1.96e-02;
Matches 11; Conservative 9; Mismatches 14; Indels 2; Gaps 2;

Db 381 GMLADGNHQAAGCCD-STGC-PGVGSAAPYGVQW 414
: : : : : : : : : : : : : : : : : : : :
QY 1 SMFPVQGPADICCCCKNGDCGTPSHSRQPHVMSQW 36

RESULT 11 PRELIMINARY; PRT; 414 AA.
AC Q90357;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ZONA PELLUCIDA PROTEIN ZP3 (FRAGMENT).
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Cyprinus.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Ovary:
RA CHANG Y., WANG S., TSAO C., HUANG F.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
DR EMBL: Z48798; CA88735.1;
DR PFM: PFM0100; zona_pellucida.1.
FT NON_TER 1
SO SEQUENCE 414 AA; 45106 MW; B919EBF0 CRC32;

Query Match 24.6%; Score 80; DB 13; Length 414;
Best Local Similarity 30.6%; Pred. NO. 3.03e-02;
Matches 11; Conservative 9; Mismatches 14; Indels 2; Gaps 2;

Db 373 GMLADGNHQAAGCCD-STGC-PGVGSAAPYGVQW 406
: : : : : : : : : : : : : : : : : : : :
QY 1 SMFPVQGPADICCCCKNGDCGTPSHSRQPHVMSQW 36

EESULT 12 PRELIMINARY; PRT; 419 AA.
AC Q92017;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE ZP3 GENE.
GN ZP3.
OS Cyprinus carpio (Common carp).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
OC Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Cyprinidae; Cyprinidae; Cyprinus.
RN [1]
RP SEQUENCE FROM N.A.
RA CHANG Y., WANG S., TSAO C., HUANG F.;
RL Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
SQ SEQUENCE FROM N.A.
RA CHANG Y.S., WANG S.C., TSAO C.C., HUANG F.L.;

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[illegible]

Search completed: Fri Apr 28 14:25:46 2000
 Job time : 81 secs.

BA PARSONS J., PERCY C., RIEKEN L., ROOPRA A., SAUNDERS D., SHOWNKEEN R.,
 BA SMADON N., SMITH A., SONNHAMER E., STADEN R., SULSTON J.,
 BA THIERRY-MIEG J., THOMAS K., VAUDIN M., VAUGHAN K., WATERSTON R.,
 BA WATSON A., WEINSTOCK L., WILKINSON-SPROAT J., WOLDMAN P.,
 FT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
 elegans.";
 FL Nature 368:32-38(1994).

[2]
 SEQUENCE FROM N.A.

AP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;

RA GOELA D.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.

[3]
 SEQUENCE FROM N.A.

RC STRAIN-BRISTOL N2;
 RA WATERSTON R.;

RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 CR EMBL: AF022979; AAB69903.1; -

SEQ SEQUENCE 295 AA; 34613 MW; B7BEDAB CRC32;

Query Match

Best Local Similarity 23.1%; Score 75; DB 5; Length 295;
 Matches 7; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

DB 91 FHVOSASTICICCHR 105

QY 3 FVVGPADICCCCNK 17

Result 15

PRELIMINARY; PRT; 843 AA.

ID O9XARO.

DI 01-NOV-1999 (TRENBLREL. 12, Created)

DI 01-NOV-1999 (TRENBLREL. 12, Last sequence update)

DI 01-NOV-1999 (TRENBLREL. 12, Last annotation update)

DE NUOG, NADH DEHYDROGENASE SUBUNIT.

OS Streptomyces coelicolor.
 CC Bacteria; Filicutes; Actinobacteria; Actinobacteridae;
 CC Actinomycetales; Streptomycetaceae; Streptomyces.

RM [1]
 SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 RA SAUNDERS D.C., HARRIS D.;

RL "A set of ordered cosmid and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RM [2]
 SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 RA BENTLEY S.D., PARKHILL J., BARRELL B.G., RAJANDREAM M.A.;

RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.

RM [3]
 SEQUENCE FROM N.A.

RC STRAIN-A3(2);
 RA MEDLINE; 97000351.
 RA REDENBACH M., KIESER H.M., DENAPATE D., EICHNER A., CULLUM J.,

RA KINASHI H., HOPWOOD D.A.;
 RA "A set of ordered cosmid and a detailed genetic and physical map for
 the 8 Mb Streptomyces coelicolor A3(2) chromosome.";

RL Mol. Microbiol. 21:77-96(1996).

DR EMBL: AL078618; CAB44525.1; -

SEQ SEQUENCE 843 AA; 88861 MW; 53EF1405 CRC32;

Query Match 23.1%; Score 75; DB 2; Length 843;
 Best Local Similarity 32.3%; Pred. No. 2.54e-01;
 Matches 10; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

DB 236 FDLISSPSVCEHC-GGCAFRIDHRR-GKYM 264

QY 3 FVVGPADICCCCNKGGCTPSHRRPHYM 33

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